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Matches 542; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 543 AA;
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activity. The heparanase (hpa) polynucleotide is useful in gene therapy particularly in treating tumour, inflammation or autoimmunity. Particularly, the polynucleotide is useful in modulating the particularly, the polynucleotide is useful in modulating the bioavailability of heparin-binding growth factors, cellular responses the heparin-binding growth factors (e.g. bFGF) and cytokines (e.g. interleukin (II)-8), cell interaction with plasma lipoproteins, cellula susceptibility to certain viral and some bacterial and protozoa infections, or disintegration of neurodegenerative plaques. The polynucleotide is also useful in wound healing (e.g. thermal, chemical radiation burns), and in the treatment of angiogenesis, restenosis, atherosclerosis, inflammation, neurodegenerative diseases (Gerstmann-Straussler Syndrome or Creutzfeldt-Jakob disease), and some viral,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QLGEDYIQLHKLLRKSTFKNAKLYGPDVGQPRRKTAKMLKSFLKAGGEVIDSVTWHHYYL
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                                                                                                                                                                                                                                                                                                                                                                                                                   protein;
                                                                                                                                                                                                                                                                                                     entry
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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NGRTATREDFLNPDVLDIFISSVQKVFQVVESTRPGKKVWLGETSSAYGGGAPLLSDTFA

QLGEDFIQLHKLLRKSTFKNAKLYGPDVGQPRRKTAKMLKSFLKAGGEVIDSVTWHHYYL

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QLGEDYIQLHKLLRKSTFKNAKLYGPDVGQPRRKTAKMLKSFLKAGGEVIDSVTWHHYYL

GLDLIFGLNALLRTADLQWNSSNAQLLLDYCSSKGYNISWELGNEPNSFLKKADIFINGS QVNQDICKYGSIPPDVEEKLRLEWPYQEQLLLREHYQKKFKNSTYSRSSVDVLYTFANCS

GLDLIFGLNALLRTADLQWNSSNAQLLLDYCSSKGYNISWELGNEPNSFLKKADIFINGS

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                                                                                                                                                                                                                                                                                              The present invention describes genetically modified cells (A) containing CC a polynucleotide (I) that encodes a polypeptide with heparanase activity, CC and express recombinant heparanase (II). Heparanase cleaves heparan CC sulphate (HS) at specific intrachain sites, resulting in release of the parin-binding growth factors, enzymes and proteins that are sequestered CC by HS in basement membranes, extracellular matrix or cell surfaces. It CC may also be implicated in tumour angiogenesis and metastases. (II) is CC potentially useful in wound healing and for treating angiogenesis, CC restenosis, atherosclerosis, inflammation, neurodegeneration, viral CC infection and cystic fibrosis. It can also be used to neutralise heparin CC (an alternative to protamine) and to screen for specific inhibitors (potentially useful for treating cancer and metastases). Antibodies CC raised against (II) are used for immunodetection and diagnosis of CC raised against (II) are used for immunodetection and diagnosis of CC in large quantities, in a form that is homogeneously processed and CC activated/neutralised by a dedicated protease. The present sequence
                                                                                                                                                                                Query Match
Best Local S
Matches 542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Engineered cells that express recombinant heparanase, useful therapeutically, e.g. for treating angiogenesis and to scree specific inhibitors, potential anticancer agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (INSI-)
(FRIE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB;
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02-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                     represents human heparanase
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542; Conserv
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QVNQDICKYGSIPPDVEEKLRLEWPYQEQLLLREHYQKKFKNSTYSRSSVDVLYTFANCS
                                             IDANLATDPRFLILLGSPKLRTLARGLSPAYLRFGGTKTDFLIFDPKKESTFEERSYWQS
                                                                 IDANLATDPRFLILLGSPKLRTLARGLSPAYLRFGGTKTDFLIFDPKKESTFEERSYWQS
                                                                                                               MLLRSKPALPPPLMLLLLGPLGPLSPGALPRPAQAQDVVDLDFFTQEPLHLVSPSFLSVT
                                                                                                                                  MLLRSKPALPPPLMLLLLLGPLGPLSPGALPRPAQAQDVVDLDFFTQEPLHLVSPSFLSVT
                                                                                                                                                                                                                                                     543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Page 107-109; 118pp;
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                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                     AA;
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99US-00260038.
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                                                                                                                                                                                                99.9%;
                                                                                                                                                                                Score 2838; DB 3;
Pred. No. 5.3e-275;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              English.
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20-MAR-2003 14-OCT-1999

(revised) (first entry)

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The present sequence represents a polypeptide with human heparanase CC biological activity. Antagonists and inhibitors of the protein prevent it CC from degrading the extracellular matrix and releasing heparan sulfate CC from the extracellular matrix surface. The heparanase protein or the anti CC expression of the heparanase protein, or from excessive activity or over-CC lack of the heparanase protein, or from excessive activity or over-CC expression of the heparanase protein, respectively. The heparanase cC expression of the heparanase protein, respectively. The heparanase CC including Alzheimer's diseases such as trauma, autoimmune disease, CC golypeptide. The anti-heparanase antibody is used in treating the CC diseases like cancer, cancer metastasis, anglogenesis and inflammation of heparanase protein. The anti-heparanase activity or over expression of heparanase protein. The anti-heparanase antibody can be used to detect the presence or absence of polypeptide and its concentration. (Updated on CC 20-MAR-2003 to correct PA field.)
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Best Local S
Matches 543
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New heparanase polypeptide useful for treating autoimmune diseases, skin diseases, cardiovascular diseases and nervous system diseases including
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 3; Page 29-31; 40pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alzheimer's disease.
                                                                                                                                                                                                                                                                                                  Sequence 588 AA;
                            181
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 226
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NOVARTIS-ERFINDUNGEN VERW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein with heparanase activity.
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                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                               MLLRSKPALPPPLMLLLLGPLGPLSPGALPRPAQAQDVVDLDFFTQEPLHLVSPSFLSVT
                 GLDL1FGLNALLRTADLQWNSSNAQLLLDYCSSKGYNISWELGNEPNSFLKKADIFINGS
                                                                           MLLRSKPALPPPLMLLLLGPLGPLSPGALPRPAQAQDVVDLDFFTQEPLHLVSPSFLSVT
GLDLIFGLNALLRTADLQWNSSNAQLLLDYCSSKGYNISWELGNEPNSFLKKADIFINGS
                                                          QVNQDICKYGSIPPDVEEKLRLEWPYQEQLLLREHYQKKFKNSTYSRSSYDVLYTFANCS
                                                                                                                      IDANLATDPRFLILLGSPKLRTLARGLSPAYLRFGGTKTDFLIFDPKKESTFEERSYWQS
                                                                                                                                        Conservative
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                                                                                                                                                                                                                                          Score 2841; DB 2; Pred. No. 3e-275; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cellular response; cytokine; cell interaction; plasma lipoprotein; cellular susceptibility; infection; disintegration; neurodegenerative plaque; wound healing; angiogenesis; restenosis; atherselerosis; inflammation; neurodegenerative disease; neutralise; plasma heparin; micrometastasis; autoimmune lesion; renal failure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Heparanase; hp; modulator; heparin-binding growth factor; cellular response; cytokine; cell interaction; plasma lipoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A human heparanase protein
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02-JUL-1998;
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The specification describes a polypeptide having heparanase (hp) activity. The recombinant protein is used as a modulator of heparin-binding growth factors, cellular responses to heparin-binding growth factors cell interaction with plasma lipoproteins, cellular susceptibility to viral, protozoal and bacterial infections

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                 The invention relates to a novel isolated nucleic acid and the PRO polypeptide encoded by it. A protein of the invention has antiinflammatory, antiarthritic, antirheumatic, immunosuppressive, osteopathic, antidiabetic, dermatological, antipsoriatic, antiallergic, antiasthmatic, hepatrotropic, and respiratory activity. A polynucleotide of the invention may have a use in gene therapy. The PRO polypeptide, it agonist, antagonist, or antibody that specifically binds to the polypeptide is useful for treating an immune related disorder such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRO; antiinflammatory; antiarthritic; antirheumatic; immunosuppressive; osteopathic; antidiabetic; dermatological; antipsoriatic; antiallergic; antiasthmatic; hepatotropic; respiratory; gene therapy; immune system.
                                                                                                                                                                                                                                                                                                                                                 New PRO polypeptides and polynucleotides, useful for treating e.g. erythematosus, rheumatoid arthritis, diabetes mellitus, immune-mediated renal disease, or demyelinating diseases of the central or peripheral
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                                                                     RPLGPHGLLSKSVQLNGLTLKMVDDQTLPPLMEKPLRPGSSLGLPAFSYSFFVIRNAKVA
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Pred. No. 2.7e-275;
; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human preproheparanase
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                                                                                                                                                                                                                                                                                         Active-site
                                                                                                                                                                                                                                                                                                                                               Domain
                                                                                                                                                                                                                                                                                                                                                                Region
                                                                                                                                                                                                                                                                                                                                                                                  Protein
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                                                                                  02-SEP-1997;
01-MAY-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                  Peptide
                                                                                                              28-NOV-2003;
                  (MIRO/)
                             (PERE/
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PERETZ T.
MIRON D.
SHLOMI Y.
PECKER I.
                           YACOBY-ZEEVI
PERETZ T.
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2003US-00645659
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98US-00071739.
98US-00186200.
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437. .4
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CC capable of specifically printing to at teast one curvature of composition and methods of the invention are useful for controlled. The composition and methods of the invention are useful for catalytic activity (e.g. an inflammatory disorder, wound, scar, catalytic activity) an autoimmune disorder, cancer, angiogenesis, cell controlled to those conditions of carcerous condition and metastatic conditions. The vasculopathy is atherosclerosis, crestenosis or aneurysm. The cancerous condition is a solid cancer or a connected from acute lymphocytic leukaemia (CLL), chronic myelogenous conditions is a haematopoietic malignancy ce selected from acute lymphocytic leukaemia (CLL), chronic myelogenous conditions disease, non-Hodgkin's lymphomas, mat cell leukaemia, (CLM), myelodysplastic syndrome (MDS), mast cell leukaemia, cerdity, myelodysplastic syndromes, material tumours in lip and coral cavity, pharynx, plarynx, paranasal sinuses, major salivary glands, cerdity uteri, ovary, fallopian timestine, colon, colorectum, canal, liver, gallbladder, extrahepatic bile ducts, ampulla of colorectum, carcinoma and malignant melanoma of the skin, breast, vulva, carcinoma of the conjunctiva, melignant melanoma of the conjunctiva, certinoblastoma, carcinoma of the conjunctiva, melignant melanoma of the conjunctiva, retinoblastoma, carcinoma of the conjunctiva, melignant melanoma of the conjunctiva, retinoblastoma, carcinoma of the lacrimal gland, sarcoma of the orbit, carcinoma and kaposi's coral present sentence is human preprobleparanase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Targeted drug delivery to a heparanase-expressing tissue of a patient, useful for treating heparanase-associated conditions such as inflammation or cancer, comprises administering a drug and an anti-heparanase antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of a patient, the tissue expressing heparanase. The method comprises providing a complex of a drug directly or indirectly linked to an antiheparanase antibody, and administering the complex to the patient. In the targeted drug delivery, the antibody comprises an antibody or its portion capable of specifically binding to at least one epitope of a heparanase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a method of targeted drug delivery to a tissue of a patient, the tissue expressing heparanase. The method comprises
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 2;
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Ayal-Hershkovitz
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(FEIN/)
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                                            spinal cord, vascular and the present sequence
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) VAN GELDER J
) VLODAVSKY I.
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FRIEDMANN Y.
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M, Feinstein E,
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                                               is human preproheparanase.
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n Gelder JM,
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, Vlodavsky
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Š Ş 맒 밁 뮍 Ş Query Match Best Local 121 121 543; 61 61 1 MILRSKPALPPPLMLLLLGPLGPLSPGALPRPAQAQDVVDLDFFTQEPLHLVSPSFLSVT Similarity QVNQDICKYGSIPPDVEEKLRLEWPYQEQLLLREHYQKKFKNSTYSRSSVDVLYTFANCS IDANLATDPRFLILLGSPKLRTLARGLSPÄYLRFGGTKTDFLIFDPKKESTFEERSYWQS MILRSKPALPPPLMLLLLGPLGPLSPGALPRPAQAQDVVDLDFFTQEPLHLVSPSFLSVT QVNQDICKYGSIPPDVEEKLRLEWPYQEQLLLREHYQKKFKNSTYSRSSVDVLYTFANCS IDANLATDPRFLILLGSPKLRTLARGLSPAYLRFGGTKTDFLIFDPKKESTFEERSYWQS Conservative 100.0%; <u>.</u> Score 2841; DB 8; Pred. No. 2.7e-275; Mismatches 0; Length Indels 543; 0; Gaps

120

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Sequence 543 AA;

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GLDLIFGLNALLRTADLOWNSSNAOLLLDYCSSKGYNISWELGNEPNSFLKKADIFINGS

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LOWNSSNAOLLLDYCSSKGYNISWELGNEPNSFLKKADIFINGS

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Best Local Similarity 100.0%;
Matches 543; Conservative
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                                    WO2004063709-A2
                                                            Homo sapiens
                                                                                      cytostatic;
therapeutic
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                                                                                                                                                                                                        protein;
                                                                                      growth factor receptor modulator;
cancer; EGFR; biomarker.
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Pred. No. 2.7e-275;
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Identifying a mammal that will respond therapeutically to a method of treating cancer comprises comparing the level of a biomarker in a mammal before and after exposure to an epidermal growth factor receptor (EFGR)
                                                                                                                        Disclosure;
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                                                                                                                                                                                                                                   08-JAN-2004; 2004WO-US000368
                                                                                                                                                                                                        (BRIM ) BRISTOL-MYERS SQUIBB CO
                                                                                                                                                                                          ŗ,
                                                                                                                        SEQ ID
                                                                                                                       NO 144;
                                                                                                                        520pp;
                                                                                                                        English.
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The invention relates to a method of identifying a mammal that will CC respond therapeutically to a method of treating cancer by administering CC an epidermal growth factor receptor (EGFR) modulator by comparing the CC level of a biomarker in a mammal before and after exposure to an EGFR cC modulator. The method comprises: (a) measuring, in the mammal, the level CC for at least one biomarker identified in the specification; (b) exposing CC the mammal to the EGFR modulator; and (c) measuring in the mammal the CC level of the biomarker, where a difference in the level in step (c) CC compared to step (a) indicates that the mammal will respond CC therapeutically to the method of treating cancer. The method and CC therapeutically to a method of treating cancer by administering an CC epidermal growth factor receptor (EGFR) modulator. This sequence CC corresponds to one of the biomarkers whose levels of expression is CC measured in the method of the invention.

Sequence 543 **A**

Query Match Best Local S Matches 543

Similarity

100.0%; Score 2841; DB 8; ilarity 100.0%; Pred. No. 2.7e-275; Conservative 0; Mismatches 0;

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                 ASVQGSKRRKLRVYLHCTNTDNPRYKEGDLTLYAINLHNVTKYLRLPYPFSNKQVDKYLL
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Matches 543
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N-PSDB; ADN05073.
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                                                                                                                                                                                             The invention relates to novel polynucleotide and polypeptides for treating psoriasis or a sequence having at least 80% identity to the above sequences. The nucleic acid is useful for preparing a composition for diagnosing or treating psoriasis in a mammal. This sequence corresponds to one of the polypeptides of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                    New PRO nucleic acid or polypeptide, useful for preparing a pharmaceutical composition for diagnosing or treating psoriasis
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                                                                                                                                                                                                                                                                                                                                   Claim 9; SEQ ID NO 1468; 3069pp; English.
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                                     c acid or polypeptide, useful for preparing a composition for diagnosing or treating psoriasis
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Best Local
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                                 Human hpa protein #2
   Transgenic animal; heparanase; cancer; viral infection; restenosis;
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Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                   genome comprises an exogenous polynucleotide sequence, including a promoter active in tissues of the non-human, a region encoding a human heparanase, where the promoter and the region encoding human heparanase are operably linked in the exogenous polynucleotide such that human heparanase is expressed in at least a portion of the cells of the non-human animal. The methods and compositions of the present invention are useful for the production of transgenic animals expressing heparanase, to be used as models for human diseases such as cancers, viral infection, restenosis, neurodegenerative diseases, atheroselerosis and pulmonary disorders. The present sequence is human hpa protein used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New transgenic non-human animal expressing heparinase, useful for human disease, such as cancers, viral infection, neurodegodiseases, restenosis, atherosclerosis and pulmonary disorders
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19-NOV-2001;
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01-MAR-1999;
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Goldshmidt
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Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                           CC This invention relates to novel human genes and gene product which are cc implicated in certain disease states. Compounds which modulate the CC proteains of the invention may have cytostatic, antiinflammatory, CC ophthalmological, antiarteriosclerotic or vulnerary activities. The CC sequences of the invention may be useful for gene therapy. The invention cc such as tumourigenesis, angiogenesis, apoptosis, inflammation, CC such as tumourigenesis, angiogenesis, apoptosis, inflammation, CC erythropoiesis, or the biological response to hypoxia conditions CC including processes such as glycolysis, gluconeogenesis, glucose CC transportation, catecholamine synthesis, iron transport or nitric oxide CC synthesis. The disease includes cancer, ischaemic conditions, reperfusion CC injury, retinopathy, neonateal stress, pre-eclampsia, atherosclerosis, CC inflammatory conditions or wound healing. The present sequence is that of CC a disease related protein of the invention.
                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 543; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New substantially purified polypeptide, useful for diagnosing or treating a hypoxia-regulated condition, such as cancer, ischemia, reperfusion injury, retinopathy, pre-eclampsia, atherosclerosis, inflammation, or wound healing.
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                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 25; SEQ ID NO 439; 424pp; English.
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05-OCT-2001; 2001GB-00024037.
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                                                                                                                                                                                                                                                                                                                            543 AA;
      IDANLATDPRFLILLGSPKLRTLARGLSPAYLRFGGTKTDFLIFDPKKESTFEERSYWQS
                                                               MLLRSKPALPPPLMLLLLGPLGPLSPGALPRPAQAQDVVDLDFFTQEPLHLVSPSFLSVT
                                                                                                                                                                                              Conservative
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                                                                                                                           N-PSDB; ADK51968
                                                                                                                                                                                                 Mitsuishi
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UNIV JUNTENDO.
                                                                                                                                                                                              Ogawa K,
i K;
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Detecting atopic dermatitis or psoriasis comprises assaying levels of expression of an indicator gene at a rash site and non-rash site of a person with atopic dermatitis or psoriasis.

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                                                   DE19955803-A1
                                                                            Homo
                                                                                                   Heparanase; inhibitor; cardiac insufficiency; cardiant; nephrotropic; heparotropic; veterinary medicine; congestive heart failure; dyspnoea primary cardiomyogathy; peripheral odema; pulmonary congestion; hepatic congestion; hydrothorax; ascite; nocturia; human.
                                                                                                                                                                                            24-AUG-2001
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Pred. No. 2.7e-275;
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This invention describes a novel heparanase inhibitor which can be used for the treatment or prevention of cardiac insufficiency and associated indications, symptoms and/or malfunctions. The heparanase inhibitor of the invention has cardiant, nephrotropic and hepatotropic activity. The products of the invention can be used in human and veterinary medicine, for the treatment or prevention of congestive heart failure e.g. primary cardiomyopathy. Associated conditions treated or prevented with the inhibitor are especially peripheral odemas, pulmonary and hepatic congestion, dyspnoea, hydrothorax and ascites. Renal problems, e.g. nocturia can also be treated. This sequence represents the human heparanase protein described in the method of the invention
                                                                                                                                                                                                                                                                                                              Treatment or prevention e.g. pulmonary congestic
Sequence 543 AA;
                                                                                                                                                                                                                                                         Disclosure; Page 11-13; 16pp; German
                                                                                                                                                                                                                                                                                                                                                                      N-PSDB;
                                                                                                                                                                                                                                                                                           heparanase inhibitor.
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Ś 문 S 밁 Ş 5 밁 δ 밁 δ 밁 Ş 밁 δ 밁 밁 밁 S Query Match Best Local Simi Matches 543; 481 481 421 421 361 361 301 301 241 241 181 181 121 121 19 61 Н Similarity RPLGPHGLLSKSVQLNGLTLKMVDDQTLPPLMEKPLRPGSSLGLPAFSYSFFVIRNAKVA NGRTATREDFLNPDVLDIFISSVQKVFQVVESTRPGKKVWLGETSSAYGGGAPLLSDTFA GLDL1FGLNALLRTADLQWNSSNAQLLLDYCSSKGYNISWELGNEPNSFLKKADIFINGS GLDLIFGLNALLRTADLQWNSSNAQLLLDYCSSKGYNISWELGNEPNSFLKKADIFINGS QVNQDICKYGSIPPDVEEKLRLEWPYQEQLLLREHYQKKFKNSTYSRSSVDVLYTFANCS IDANLATDPRFLILLGSPKLRTLARGLSPAYLRFGGTKTDFLIFDPKKESTFEBRSYWQS MLLRSKPALPPPLMLLLLGPLGPLSPGALPRPAQAQDVVDLDFFTQEPLHLVSPSFLSVT MLLRSKPALPPPLMLLLLGPLGPLSPGALPRPAQAQDVVDLDFFTQEPLHLVSPSFLSVT ASVQGSKRRKLRVYLHCTNTDNPRYKEGDLTLYAINLHNVTKYLRLPYPFSNKQVDKYLL AGFMWLDKLGLSARMGIEVVMRQVFFGAGNYHLVDENFDPLPDYWLSLLFKKLVGTKVLM AGFMWLDKLGLSARMGI EVVMRQVFFGAGNYHLVDENFDPLPDYWLSLLFKKLVGTKVLM NGRTATREDFLNPDVLDIFISSVQKVFQVVESTRPGKKVWLGETSSAYGGGAPLLSDTFA QVNQDICKYGSIPPDVEEKLRLEWPYQEQLLLREHYQKKFKNSTYSRSSVDVLYTFANCS IDANLATDPRFLILLGSPKLRTLARGLSPAYLRFGGTKTDFLIFDPKKESTFEERSYWQS RPLGPHGLLSKSVQLNGLTLKMVDDQTLPPLMEKPLRPGSSLGLPAFSYSFFVIRNAKVA ASVQGSKRRKLRVYLHCTNTDNPRYKEGDLTLYAINLHNVTKYLRLPYPFSNKQVDKYLL 100.0%; S ilarity 100.0%; P Conservative 0; Score 2841; DB 4; Pred. No. 2.7e-275; Mismatches 0; Length Indels 543; 0 Gaps 120 540 480 420 420 360 360 300 180 120 60 480 300 240 180 240 0

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Copyright
 GenCore version (c) 1993 - 2005
Compugen Ltd.
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OM protein - protein search, using sw model

Run on: March 23, 2005, 11:09:57 ; Search time 113.5 Seconds (without alignments) 1850.316 Million cell updates/sec

Perfect score: Title: SEQ2B 2841 1 MLLF

Scoring table:

BLOSUM62

MLLRSKPALPPPLMLLLLGP......LPAFSYSFFVIRNAKVAACI 543

2105692 seqs, 386760381 residues Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters:

2105692

Maximum Minimum 80 80 seq length: 0 length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database A_Geneseq_16Dec04:*
1: geneseqp1980s:* geneseqp2001s:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES

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ALIGNMENTS

AAY17082 standard; protein; 543 A.

AAY17082;

21-JUL-1999 (first entry)

Human heparanase enzyme.

Heparanase; endoglucuronidase; heparan sulfate proteoglycan; enzyme; metastasis; angiogenesis; wound healing; angioplasty-induced restenosis; arteriosclerosis; atherosclerosis; inflammation; tissue development; HSPG.

Homo sapiens.

WO9921975-A1

06-MAY-1999

28-OCT-1997; 09-DEC-1997; 28-OCT-1998; 97AU-00000062. 97AU-00000812. 98WO-AU000898

(AUSU) UNIV AUSTRALIAN NAT.

Freeman CG, Hulett MD, Parish œ, Hamdorf

WPI; 1999-312956/26.

N-PSDB; AAX37259

Polynucleotides encoding mammalian endoglucuronidases, especially heparanases, useful to promote wound healing.

Claim 6; Page 69-73; 112pp; English.

The invention relates to nucleic acid sequences that encode heparanase enzymes having endoglucuronidase activity. Recombinant heparanases are capable of removing the HS side chain from heparan sulfate proteoglycan (HSPG). Sulfated oligosaccharides, sulphonates or HSPG can be used to inhibit heparanase, this is useful for treatment of a physiological or medical condition associated with elevated heparanase activity, such as metastasis, angiogenesis, wound healing, angioplasty-induced restenosis, arteriosclerosis, atherosclerosis and inflammation. The human, murine and rat heparanases can be used to enhance wound healing, especially associated with tissue development and repair. The conditions mentioned

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, pp	Qy Db Db	RESULT 15 AI1489 probable [C;Species 2 C;Date: 2 C;Date: 2 C;Cancessing D; Jones Science 2 A;Authors Ok, C; Sc A;Title: C; Sc A;Title: C, Sc A;Moleculal A;Referen A;Residue A;Experime C;Genetic A;Gene: 11	D
369 FĞEPYWSQLSTVNGKANVLVNDDEKQVVEYĞPİNANIYQRIQVS 412 144 WP	SKPALPPPLMILLLGPLGPLSPGALPRPAQAQDVVDLDFFT 4	Listeria innocu Listeria innocu -Nov-2001 #seque P.; Frangeul, L. L.M.; Karst, U. L.M.; Karst, U. A49-852, 2001 Kreft, J.; Kuhr hlueter, T.; Sin chlueter, T. Sin chlueter, T. Sin hlueter, T.	27 GALPRPAQAQDVVDLDFFTQEPLHLVSPSELSVTIDANLATDPRF-LILLGSPKLRT 82

Search completed: March 23, 2005, 11:31:41 Job time : 29 secs

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adenylosuccinate synthetase - C;Species: Aquifex aeolicus C;Date: 08-May-1998 #sequence_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Accession: S00652; T40496; T40422
R;McKenzie, R.; Schuchert, P.; Kilbey, B.
Curr. Genet. 12. 591-597, 1987
A;Title: Sequence of the bifunctional adel
A;Reference number: S00652; MUID:89003164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 604-788 <SEE>
A;Cross-references: EMBL:AL035655; PIDN:CAB38600.1; GSPDB:GN00067; SPDB:SPBC405.01
A;Experimental source: strain 972h-; cosmid c405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Experimental source: strain 972h-; cosmid c4C3
R;Seeger, K.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell,
submitted to the EMBL Data Library, March 1999
A;Reference number: Z21928
A;Accession: T40422
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C;Date: 07-Sep-1990 #sequence_revision 28-Oct-1994 #text_change 09-Jul-2004
C;Accession: S00652; T40496; T40422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross.references: EMBL:AL021730; PIDN:CAA16823.1; GSPDB:GN00067; SPDB:SPBC4C3.02c
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A; Residues: 1-788 < WOO>
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A; Accession: T40496
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Residues: 1-788 < MCK>
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                                                                                                           RESULT 13
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hes 70; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -GGGAPLL-SDTFAAGFMWLDKLGLSAR--MGIEVVMRQVFFGAGNYHLVDENFDPL--P
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                                                                                                                                                                                    RLGDSLLIPTRIY
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                                                                                                                                                                                                                                                                                                                                                                                                                                      DYWLSLLFKKLVGTKVLMASVQGSKRRKLRVYLHCTNTDNPRYKEGDLTLYAINLHNVTK 462
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       #sequence_revision
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3.7%; Score 104.5;
27.7%; Pred. No. 14;
tive 36; Mismatches
                                                       Aquifex aeolicus
                                                                                                                                                                                                                                                                                      GLASDGVHSNGYSLVRKIVEYSDLEYTSVCPWDKNV
          08-May-1998
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     #text_change 09-Jul-2004
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     Query Match
Best Local S
Matches 77
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C;Genetics:
A;Gene: CAC1343
C;Superfamily: I
                                                                                                                                              transketolase (imported) - Clostridium acetobutylicum (;Species: Clostridium acetobutylicum C;Species: Clostridium acetobutylicum C;Date: 114-Sep_2001 #sequence_revision 14-Sep_2001 #text_change 09-Jul-2004 C;Accession: D97065 R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gib; R;Nolling, J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R. ; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R. J. Bacteriol. 183, 4823-4838, 2001 A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing 1A;Reference number: A96900; MUID:21359325; PMID:21359325 A;Accession: D97065 A;Status: preliminary p.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Residues: 1-432 <AQF>
A;Cross-references: UNIPROT:067321;
A;Experimental source: strain VF5
C;Genetics:
A;Gene: purA
C;Superfamily: adenylosuccinate synt
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A;Accession: F70411
A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
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R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham,
                                                                   A;Cross-references: UNIPROT:Q97JE3;
A;Experimental source: Clostridium a
                                                                                                            A; Molecule type: DNA
A; Residues: 1-796 < KUR>
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    phosphoketolase
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Pred. No. 6.
                                                                   GB:AE001437; PIDN:AAK79311.1; acetobutylicum ATCC824
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                                                                                        PID:g15024275;
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Similarity 77; Conserv

Conservative

51;

Mismatches

114;

Indels

114;

Gaps

18;

21.6%; 3.7%;

Score 104; Pred. No.

DB

2

Length 796;

GSPDB:GI

a

92

genon

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A;Accession: S74760
A;Status: preliminary
A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-411 <KAN>
A;Cross-references: UNIDROT:P72895; EMBL:D90901; GB:AB001339; NID:g1651897; PIDN:BAA1691
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein slr1617 - Synechocystis sp. (strain PCC 6803)
C;Species: Synechocystis sp.
A;Variety: PCC 6803
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: S74760
C;Accession: S
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Best Local
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                                                                                                                                                                                                                                                                                                                             207 LLDYCSSKG----YNISWEL-----GNEFNSFLKK-----ADIFINGSQLGE 244
                                                                                                                                                                                                                                                                                                                                                                                                                      159 KFKNSTYSRSSVDVLYTFANCSGLDLIF---GLNALLRTADLQWNSSNAQL------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -LVKIPKNPFSEKLTISNVNRYLNIVPGSLDLQFSLTNENF----VHWNSTVYQELLNLK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FLRSK---NSIEKPRNFRREKFLKKFLAMQKEIKYLRKRKLQIRKIPNYKYSDRSLNSKT
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                                           AGFMWLDKLGLSA-----RMGIEVVMRQVFFGAGNYHLVDENFDPLPDYWLSLLFKKLVG 415
                                                                                                                                                                                                                                 DFIQLHKLLRKSTFKNAKLYGPDVGQPRRKTAKMLKSFLKAGGEVIDSVTWHHYYLNGRT 304
                                                                                                                                                                                                                                                                                 VIDVCLAKDIPLIYPSSWEIYSGYAGTIHADESTPALPRGPYGETKYLAEILI------
                                                                                                                                                                                                                                                                                                                                                                        EFRLISPTREQIDI---FAGSTKLDLLASEENIDCIVHLANPRVYTSNVAMGQTLTMLRN
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IAEMIRDELGSSSMIQQIEVNTEVASIAMNYGRAN-HVLD--
                                                                                                                                       ATREDFLNPDV----LDIFISSVQKVFQVVESTRPGKKVWLGETSSAYGGGAPLLSDTFA 360
                                                                                                                                                                                       DHCRRTRGLRCAILRSSPVYGSMSDKP-----KFIFNFFKKASQGQKIVT--HHYING--
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4; Mismatches
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A;Residues: 1-879 <-HAY
A;Cross-references: UNIPROT:Q8XCP4; GB:BA000007;
A;Experimental source: strain O157:H7, substrain C;Genetics:
A;Gene: EC83221
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       GVYISLSMPWGDSSTISY----NGNYGSGSDSSQVG--YFSRVDDAT
                                                                                                NFRDAGVSVYLNYTRHTYWDRDEQTNYNVMLSHYFNLGSIRNMSISMTGYRYEYDNQADK
                                                                                                                                                                                                                                                                                      SLYGGA---LADEHYQSAALGVGRDLSVFGAVAFDITHSHTRLDKETAYGKGSLDGNSFR
                                                                                                                                                                                                                                                                                                                                 SAYGGGAPLLSD------TFAA-----GFMWLDKL-----
                                                                                                                                                                                                                                                                                                                                                                               GQVQEYDINTASMPF----LTRPGQVRYKLMMGRPQEWGHHVEGGFFSGGEASWGIANGW 402
                                                                                                                                                                                                                                                                                                                                                                                                                             PDVLDIFISSVQKVFQVVESTRPGK---KVWL-----
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                                                  --YLRLPYPFSNKQVDKYLLRPLGPHGLLSKSVQLNGLTLKMVDDQT
                                                                                                                                              KRRKLRVYLHCTNTDNPRYKEGDLTLYAI - - - - - NLHNVTK - - - - -
                                                                                                                                                                                            LSYSKDFDELNSRVTFAG---YRFSEENFMTMSEY-LDASDSEMVRTGNDKEMYTATYNO
                                                                                                                                                                                                                                     MGI-----EVVMRQVFFGAGNYHLVDENFDPLPDYWLSLLFKKLVGT----KVLMASVQGS
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C;Species: Methanococcus jannaschii
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: F64383
R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; Science 273, 1058-1073, 1996
Science 273, 1058-1073, 1996
Science 273, 1058-1073, 1996
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.A; Authors: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii A;Reference number: A64300; MUID:96337999; PMID:8688087
A;Accession: F64383
A;Accession: F64383
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A;Title:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary; nucleic acid sequence not shown; translation A;Molecule type: DNA A;Molecule type: DNA A;Residues: 1-356 <BUL> A;Cross-references: UNIPROT:Q58084; GB:U67514; GB:L77117; NID:g28263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein MJ0670 - Methanococcus jannaschii C;Species: Methanococcus jannaschii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;Map position: REV596956-595886
;Start codon: CTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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Best Local
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  er, H.; Borisjuk, L.; Heim, U.; Buchner, P.; Wobus,
Cell 7, 1835-1846, 1995
le: Seed coat-associated invertases of Fava bean co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                   387
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82;
                                                                                                                                                                                                                                                  IKKGNIPEEILKIQKEDLNSSEIIKKMRLKF 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NSFLKKADIF------INGSQLGEDFIQLHKLLRKSTFKNAKLYGPDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----VLYTFANCSGLDLIFGLNALLRTADLQWNSSNAQLLLDYCSSKGYNISWELGNEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRKYMKIYNGKNEKDIKERLIKE-----LKEEHVLVETEDGTYTLKAEDEEEMMISKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ICKY-----GSIPPDVEEKLRLEWPYQEQLLLREHYQKKFKNSTYSRSSVD------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DVKDFHIQVIKYLNSQFKNNYSTLMTSSKTQDRRKSHNMPSSILDDGNKIGMHVSPIDE- 399
                                                                                                                                                                                                                                                                                         TDNPRYKEGDLTLYA - - INLHNVTKYLRLPY
                                                                                                                                                                                                                                                                                                                                       KPNRINEVDERVIALSVIALPYRDETLSLTKDKIIEDREERREKLKEKLIKIGKYLSTKQ 316
                                                                                                                                                                                                                                                                                                                                                                                   GAGNYHLVDENFD--
                                                                                                                                                                                                                                                                                                                                                                                                                              YKRMEDN - - GVLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GDARKFIIKSDKKY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GOPRRKTAKMLKSFLKAGGEVIDSVTWHHYYLNGRTAT--REDFLNPDVLDIFISSVQKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAEIDMVEICEEVLFLTLFLDIPYKEHEIIKDKVREYFLNKIGIEYKSDYDNINLY---V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GALKEAIYKFAKPS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -YSHFIDNDEPLWRDKVYPKIYTNEQTPTPDASAIFDS--HKIYAIISLLRYYLPEKR 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FQVVESTRPGKKVWLGETSSAYGGGAPLLSDTFAAGFMWLDKLGLSARMGIEVVMRQVFF 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3.9%; Score 110.5;
21.0%; Pred. No. 1.5;
ative 49; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -STFKN--AKLYGPDVGQPRRKTAKMLKSFLKAGGEV-----IDSV 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----NVVFHDAFSPKRDPTLYTYDFL------KEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----RTATREDFLNPDVLDIFISSVQKVFQVVESTR----PGKK 338
                                                                                                                                                                                                                                                                                                                                                                                                                              -SYSSAIPFRSALVDCGFVISEKESVGRKRGITLAYKNPNF
                                                                                                                                                                                                                                                                                                                                                                                PLPDYWLSLLFKKLVGTKVLMASVQGSKRRKLRVYLHCTN 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GB:U67514; GB:L77117; NID:g2826304; PIDN:AAB98664.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -KITDL----SNPR-VLDLCSGMGYNAIAALHYNK 109
      Fava bean control
                                                                                                                                                                                                                                                                                         468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels 105;
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    both unloading
                                                                                            09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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C;Geneti
A;Gene:
A;Map po
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C;Superfamily: beta-fructofuranosidase
C;Keywords: cell wall; glycoprotein; glycosidase; hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;McDougall, R.; Wood, V.; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, December 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             microtubule-associated protein ssm4 - fission yeast (Schizosacch (Species: Schizosaccharomyces pombe C;Date: 0)-Dec-1999 #sequence_revision 03-Dec-1999 #text_change C;Accession: T38446; T00012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Reference number: Z17416; MUID:96093423; PMID:8535137
A;Accession: T12094
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                              A;Title: Microtubule-associated coiled-coil protein Ssm4 is involved A;Reference number: Z14042; MUID:97311255; PMID:9167972 A;Accession: T00012
                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary; translated from GB/EMBL/DDB:
                                                                                                                                                                                                                                                                                                                                                                                                              A; Reference number: A; Accession: T38446
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                                                                                                                                                        A;Residues:
                                                                                                                                                                                              A;Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                        R;Yamashita, A.; Watanabe, Y.; Yamamoto, Genes to Cells 2, 155-166, 1997
                                                                                                                                                                                                                                                                                             A;Cross-references: UNIPROT:042667; EMBL:AL009227; PIDN:CAA15832.1; GSPDB:GN00066; SPDB: A;Experimental source: strain 972h-; cosmid c27D7 R;Yamashita, A.; Watanabe, Y.; Yamamoto, M.
                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Residues: 1-575 < WEB>
                                                                                                                                    A;Cross-references:
                                                                                                                                                                         A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                         A;Residues:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 71
                                                                                                                 ;Genetics:
                                   Query Match
                                                                          ssm4; SPAC27D7.13c
osition: 1
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                                                                                                                                                      1-670 <YAM>
                                                                                                                                                                                                                                                                                                                                                         1-670 <MCD>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KKADIFINGSQLGEDFIQL------HKLL----RKSTFKNAKLYGP------DV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DVLYTFANCSGLDLIFGLNALLRTADLQWNSSNAQLLLDYCSSKGYNISWELGNEPNSFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DDVKKGWAGIQAIPRTVWLDSSRRQLR-QWPVEELNRLRGKQVEMKNRKLKKGGY----L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DICKYG----SIPPDV-----EEKLRLEWPYQEQLLLLR----EHYQKKFKNSTYSRSSV 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYLQNQDKYIPDKTSEDGWGGLRYDYGNFYASKSFFDPTK----NRRIIWGWANESDTKE 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KHPIHSAKRTGMWECPDFYPVSLEGKNGLD--LSMMMGNNVKHVLKNSLDITRYEYYTIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QEPLHLVS-----PSFLSVTIDANLATDPRFLILLGSPKLRTLARGLS-----P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GNNKKLSLRSL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GOPRRKTAKMLKSFLKAGGEVIDSVTWHHYYLNGRT 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TLA-----SKKLEEYTSVFFRVFKAANKHKILMCSDAKSSSLNRELYKPSFAGFVNVDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EVKGITASQADVEVTFSFSSLDKAEAFDPNWENAE---DLCAQKGSKVRGGVG--PFGLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                    EMBL:AB000269; NID:g3341860;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CV.
3.7%; Score 106; DE 21.4%; Pred. No. 8.5; tive 58; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3.8%; Score 107.5;
21.1%; Pred. No. 5.2;
ive 49; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fribo,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -FGGTKTDF-----LIFDPKKESTFEERSYW----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IDHSVVESFGVGGKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fission yeast (Schizosaccharomyces pombe)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      coat
                .5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           107;
                                   2;
                                                                                                                                    PIDN:BAA31857.1; PID:g3341861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            531
                                     Length 670;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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Best Loc Matches

Local Similarity

Conservative

149;

Indels

86;

Gaps

15;

51 LVSPSFLSVTIDANLATDDRFLILLGSPKLRTLARGLSPAYLRFGGTKTDFLIFDPK-1	RESULT 5 T10666 T10666 hypothetical protein F6E21.40 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004 C;Accession: T10666 R;Bevan, M.; Lennard, N.; Quail, M.; Harris, B.; Rajandream, M.A.; Barrell, B.G.; Banord Sequence number: Z16533 A;Accession: T10666 A;Molecule type: DNA A;Residues: 1-670 <bev> A;Cross-references: UNIPROT:Q9M090; EMBL;AL049914; GSPDB:GN00062; ATSP:F6E21.40 A;Experimental source: cultivar Columbia; BAC clone F6E21 C;Genetics: A;Gene: ATSP:F6E21.40 A;Introns: 47/3; 87/1; 123/3; 203/3; 230/2; 255/3; 284/3; 305/1; 335/3; 347/3; 370/3; 39 C;Superfamily: Schizosaccharomyces pombe negative regulator of mitosis skb1 Query Match Best Local Similarity 22.4%; Pred. No. 3.6; Matches 123; Conservative 77; Mismatches 194; Indels 156; Gaps 33;</bev>	Db 1756 IKPMRFLGYETYLAEVLQQRGLPFLAEADVSAGMTÞDVNIHLDLFSRAIHYMRKALRGG 1815 Qy 420MASVQGSKRKLRVYLHCTNTDNPRYKEGDLTLYAINLHNVTKYL 464	Qy 128 KYGSIPPDVEEKLRLWPYQEQLLLRHYQKKFKNSTYSRSVDVLYTFAN 178
p	R;Doignon, F; B R;Doignon, F; B Yeast 9, 189-199 A;Title: The com A;Reference numb A;Accession: S32 A;Status: transl A;Molecule type: A;Reference numb A;Accession: S46 A;Cross-referenc R;Aigle, M.; Bac submitted to the A;Reference numb A;Accession: S46 A;Molecule type: A;Residues: 1-68 A;Cross-referenc C;Genetics: A;Cross-referenc C;Genetics: C;Superfamily: S Ouery Match Best Local Sim Matches 67;	Db 45 Qy 52 Db 49 RESULT 6 S32961 hypotherical N;Alternate C;Species: SC;Date: 30-S C;Accession:	Ø B Ø B Ø B Ø B Ø B Ø B Ø B Ø B Ø B Ø B Ø B Ø B Ø B Ø B Ø B Ø B Ø B Ø B Ø B Ø B Ø B Ø B Ø B Ø B Ø B Ø B Ø B Ø B Ø B Ø B Ø B Ø B Ø B Ø B Ø B Ø B Ø B Ø B Ø B Ø B Ø B Ø B Ø B Ø B Ø B Ø B Ø B Ø B Ø B Ø B Ø B Ø B Ø B Ø
126 IC : 164 MA 176 FA 224 -A 217 281 QD	mmon, F.; B 9-e: The com rence numb ssion: S32 us: transl: cule type: dues: 1-68 scule to the rence numb ssion: S46 cule type: cule	456 RF 524 LP 524 LP	208 LD 197 DD 197 DD 254 RK 254 TD 311 LN 311 LN 308 KN 371 LS 371 LS 421 -A 469 PF

524 499	469 456	421 407	371 363	311 308	254 254	208 197
LPAFSYSFFV 533 : : : IPS-SYTSFI 507	PFSNKQVDKYLLRPLGPHGLLSKSVQLNGLTLKMVDDQTLPPLMEKPLRPGSSLG 523	-ASVQGSKRRKLRVYLHCTNTDNPRYKEGDLTLYAINLHNVTKYLRLPY 468 : :: :	371 ISARWGIEVVMRQVFFGAGNYHLVDENFDDLÞDYWLSLLFKKLVGTKVLM 420	LNDDVLDIFISSVQKVFQVVESTRPGKKVWLGETSSAYGGGAPLLSDTFAAGFMWLDKLG 370	254 RKSTEKNAKLYGPDVGQPRRKTAKMLKSFL-KAGGEVIDSVTWHHYYLNGRTATREDF 310	208 LDYCSSKGYNISWELGNEDNSFLKKA-DIFINGSQLGEDFIQLHKLL 253

rotein YBR259w - yeast (Saccharomyces cerevisiae)
nes: hypothetical protein YBR1727
charomyces cerevisiae
1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
12961; S46140 lation not shown mplete sequence of a 19,482 bp segment located on the right arm of chromoses: S29348; MUID:93220397; PMID:8465606 Biteau, N.; Crouzet, M.; Aigle, M. 19, 1993

nces: UNIPROT:P38338; EMBL:X70529; NID:g1907246; PIDN:CAA49923.1; PID:g2969 acclet, M.C.; Barthe, C.; Biteau, N.; Crouzet, M.; Doignon, F. he Protein Sequence Database, August 1994 mber: S45940

DNA

ces: SGD:S0000463 ;88 <AIG> 1008: EMBL:236128; NID:g536684; PIDN:CAA85222.1; PID:g536685; MIPS:YBR259w

Saccharomyces cerevisiae hypothetical protein YBR259w

ANC--IDAFTGEQVRIDGAELIWTSKYLVFSSISSAVLRLNDLQNMFSAFRPYGEEALV 280 ANCSGLDLIFGLNALLRTADLOWNSSN------AQLLLD-----YCSSKGY----- 216 MAEYSSWKWDSDDKRQLQFMYEFRMKLKECLVKFYENFDLQKSSDPLKELIIPWEKIVYV 223 CKYGSIPPDVBEKIRLEWPYQEQLLLREHYQKKFKNSTYSRSS------VDVLYT 175 3.9%; Score 111; DB 2; Length 688; milarity 22.5%; Pred. No. 3.7; Conservative 45; Mismatches 94; Indels 92; DFAHIRSLKWDSNDKVESLIRALIFNDMFPYFNKEQVDTKADGIFFLRLLRKNFKEHIN 340 -----NISWELGNEPNSFLKKA---DIF--INGSQLG--EDFIQLHKLLRK----- 255 Gaps 16;

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hypothetical protein F13G24.30 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004 C;Accession: T45608 C;Accession: T45608 R;Bevan, M.; Van Der Schueren, J.; Chuang, Y.J.; Voet, M.; Robben, J.; Volckaert, Special to the Protein Sequence Database, December 1999
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A;Introns: 53/3; 66/1; 127/2; 177/1; 256/1; 319/2; 361/2; 394/3
A;Note: F13G24.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: UNIPROT:Q9SDA1; EMBL:AL133421
A;Experimental source: cultivar Columbia; BAC clone F13G24
C;Genetics:
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A;Molecule type: DNA
A;Residues: 1-521 <BEV>
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A; Accession: T45608
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                                                                                    VSNGINVVLNAESRKKKSLLDTLKRPFSWIGSKASDGYLNREEYHLTPENGVLRSKTMVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----PFQKM-----NSGLFGFSKGCLHMKRWDELNSFLTATGAVVTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DVEEKLRLEWPYQEQLLLREHYQKKFKNS---TYSRSSV-----DVLYTFANCSGLDLIF 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LTRPLLTKAIKAFKPLRIRIGGSLQDQVIYDVGNLKT----
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NGKSLKPTATGDIPSL-EPVLRSVNSPLNVLPLSMSFIVLPNFDASAC 520
                                      NGLTLKMVDDQTLPPLMEKPLRP-GSSLGLPAFSYSFFVIRNAKVAAC 542
                                                                                                                                                                                                              SLLFKKLVGTKVLMASVQGSKRRKLRVYLHCTNTDNPRYKEGDLTLYAINLHNVTKYL-- 464
                                                                                                                                                                                                                                                                                                  YGGGAPLLSDTFAAGFMWLDKLGLSARMGIEVVMROVFFGAGNYHLVDE-NFDPLPDYWL 406
                                                                                                                                                                                                                                                                                                                                                                                        TWHHYYLNGRT--ATREDFLNPDVLDIFISSVQKVF----QVVESTRPGKKVWLGETSSA 347
                                                                                                                                                                                                                                                                                                                                                                                                                                    AELYGKDLIVLKDVINK-VYKNSWLHKPILVAPGGFYEQQWYTKLLEI---SGPSVVDVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GSQLGEDFIQLHKLLRKSTFKNAKLYGPDVGQP-----RRKTAKMLKSFLKAGGEVIDSV 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GLNALRGRHKLRGKAWGGAWDHINTQDFLNYTVSKGYVIDSWEFGNELSG--SGVGASVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GLNALLRTADLQ-----WNSSNAQLLLDYCSSKGYNI-SWELGNEPNSFLKKADIFIN 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LGSPKLRTLARGLSPAYLRFGGTKTDFLIFDPKKESTFEERSYWQSQVNQDICKYGSIPP 134
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                                                                                                                                                                     ALLWHRLMGKGVLAVQTDGPP--QLRVYAHCSK-----GRAGVTLLLINLSNQSDFTVS
                                                                                                                                                                                                                                                         YNSGGRHVSDTFIDSFWYLDQLGMSARHNTKVYCRQTLVG-GFYGLLEKGTFVPNPDYYS
                                                                                                                                                                                                                                                                                                                                             THHIYNLGSGNDPALVKKIMDPS----YLSQVSKTFKDVNQTIQEHGPWASPWVGESGGA
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                                                                                                                          ----RLPYPFS---NKQVDKYLLRP---LGPHG--LLSKSVQL 495
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A,Molecule type: DNA
A,Residues: 1-2298 <SCH>
A,Residues: 1-2298 <SCH>
A,Cross-references: UNIPROT:Q96U00; EMBL:AL355933; GSPDB:GN00116; NCSP:B8B20.20
A.Experimental source: BAC clone B8B20; strain OR74A
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submitted to the EMBL Data Library, October 1998
A;Description: The sequence of A. thaliana T2L5.
                                                                                                                                                                                                                                                                                                                                                                                                          R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; F submitted to the Protein Sequence Database, May 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein B8B20.20 [imported] - Neurospora crassa
C;Species: Neurospora crassa
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
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A; Introns: 36/2; 69/3
A; Note: T2L5.6
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A;Experimental source: cultivar Columbia
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 26-Feb-1999 #sequence_revision 26-Feb-1999 #text_change 09-Jul-2004
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A;Accession: T49648
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A; Residues: 1-190 <GEI>
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A; Map position: 6
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                                                                                 Query Match
Best Local S
Matches 114
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Best Local :
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Local Similarity 27.8%;
                                                                                                        Local Similarity
  1447
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PRVDLIERLITPSNAHKEACLINIRAWNQLARLVVSNGEGSASFRPFITWRNNVFNQILD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IVFVHMRNVVVPÁČ 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GPNGVIQREEYHLTAKDGNLHSQTMLLNGNALQVNSMGDLPPIEPIHINSTEPITIAPYS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ROSLIG-GNYGLLNTTNFTPNPDYYSALIWRQLMGRKALFTTFSGTK--KIRSYTHCA--
                                      PKLRTLARGLSPA-----YLRFGGTKTDFLIFDPKKESTFEERSYWQSQV-NQDIC
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                                                                                   Conservative
                                                                                 3.9%; Score 112; DI
19.3%; Pred. No. 19;
Live 79; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18; Score 169.5; DB 2; Length 190;
18; Pred. No. 2.4e-05;
34; Mismatches 57; Indels 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -SKSVQLNGLTLKMVDDQTLPPLMEKPLRPGSSLGLPAFS
                                                                                                                          DB 2;
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                                                                                                                            Length 2298;
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                                                                                      208;
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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 23, 2005, 11:19:33 ; Search time 27 Seconds (without alignments) 1935.026 Million cell updates/sec

Title:
Perfect score:
Sequence:

SEQ2B 2841 1 MLLRSKPALPPPLMLLLLGP......LPAFSYSFFVIRNAKVAACI 543

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

-	B89045	N	578	ω : σ	0	29
OD .	A41101		1734		100.5	28
probable membrane	S19488		1314		•	27
nitrite reductase	AG1001		847		•	26
retrotransposon li	F85188		687	٠	100.5	25
	E75119		604	ن .	100.5	24
hypothetical prote	A82913		594	٠	101	23
RhtA Rhizobactin r	A95420		746	٠	101.5	22
siderophore recept	T46821		746	3.6	101.5	21
dynein heavy chain	A38905		4644	3.6	102	20
	G02529		897	3.6	102	19
probable fimbrial	F85875		879	3.6	102	18
transcription anti	AF1153		676	3.6	103.5	17
beta-xylosidase (i	D87541		500	3.6	103.5	16
probable peptidogl	AI1489		2013	3.7	104	15
transketolase [imp	D97065		796	3.7	104	14
adenylosuccinate s	F70411		432	3.7	104	13
phosphoribosylamin	S00652		788	3.7	104.5	12
probable outer mem	E91031		879	3.7	105.5	11
hypothetical prote	S74760		411	3.7	105.5	10
microtubule-associ	T38446		670		106	9
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ALIGNMENTS

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AAGFLWLNTLGMLANQGIDVVIRHSFFDHGYNHLVDQN	351 GAPLLSDTFAAGEMWLDKLGLSARMGIEVVMRQVFFGAGNYHLVDENFDPLPDYWLSLLF 410	217 DAVTWOHCYIDGKVVKVMDFLKTRLLDTLSDQIRKIQKVVNTYTPGKKIWLEGVVTTSAG 276	KVFQVVE	157 MHGRAVNGSQLGKDYIQLKSLLQPIRIYSRASLYGPNIGRPRKNVIALLDGPMKVAGSTV 216	232 KADIFINGSQLGEDFIQLHKLLRK-STFKNAKLYGPDVGQPRRKTAKMLKSFLKAGGEVI 290		172 VLYTFANCSGLDLIFGLNALLRTADLQWNSSNAQLLLDYCSSKGYNISWELGNEPNSFLK 231		112 FEERSYWQSQVNQDICKYGSIPPDVEEKLRLEWPYQEQLLLREHYQKKFKNSTYSRSSVD 171	78 FLSLQLDPSIIHD-GWLDFLSSKRLVTLARGLSPAFLREGGKRTDFLQFQNLRNPAKSR- 135	LRFGG	18 PPACLAPGALYLALLHLSLSSQAGDRRPLPVDRAAGLKEKTLILLDVSTKNPVRTVNEN 77	20 PLGPLSPGALPRPAQAQDVVDLDFFTQEPLHLVSPS 55	<pre>/ Match 31.5%; Score 893.5; DB 2; Length 480; Local Similarity 35.8%; Pred. No. 1.4e-58; les 201; Conservative 75; Mismatches 146; Indels 139; Gaps 9;</pre>	NESULT 1 1073506 heparanase protein 2a - human C;Species: Homo sapiens (man) C;Date: 17-Nov-2000 #sequence_revision 17-Nov-2000 #text_change 09-Jul-2004 C;Date: 17-Nov-2006 C;Date: 17-Nov-2006 C;Accession: JC7506 R;McKenzie, E; Tyson, K.; Stamps, A.; Smith, P.; Turner, P.; Barry, R.; Hircock, M.; Pat Biochem. Biophys. Res. Commun. 276, 1170-1177, 2000 A;Title: Cloning and expression profiling of Hpa2, a novel mammalian heparanase family me A;Reference number: JC7506 A;Reference number: JC7506 A;Residues: 1-480 <mck> A;Residues: 1-480 <mck> A;Cross-references: UNIPROT:Q9HB39; GB:AF282885 C;Comment: This protein, a intracellular membrane-bound enzyme, has biological and theraging therapies. C;Generics: Caparin binding; membrane bound C;Keywords: heparin binding; membrane bound</mck></mck>

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                                                                                                             SLLFKKLVGTKVLMASVQGSKRRKLRVYLHCTNTDNPRYKEGDLTLYAINLHNVTKYL-- 464
                                                                                                                                                                                                      TWHHYYLNGRT--ATREDFLNPDVLDIFISSVQKVF----QVVESTRPGKKVWLGETSSA
                                                                                                                                                                                                                                                   GSQLGEDFIQLHKLLRKSTFKNAKLYGPDVGQP-----RRKTAKMLKSFLKAGGEVIDSV 293
                   NGLTLKMVDDQTLPPLMEKPLRP-GSSLGLPAFSYSFFVIRNAKVAAC 542
                                                              YNSGGRHVSDTFIDSFWYLDQLGMSARHNTXVYCRQTLVG-GFYGLLEKGTFVDNDDYYS
                                                                                                                                               YGGGAPLLSDTFAAGFMWLDKLGLSARMGIEVVMRQVFFGAGNYHLVDB-NFDPLPDYWL 406
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Submitted (JUN-2000) to the EMBL/GenBank/DDBJ
EMBL; AF282885; AAG23421.1; -.
PIR; JC7506; JC7506.
InterPro; IPR005199; Glyco_hydro_79n; T.
Pfam; PF03662; Glyco_hydro_79n; T.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                               MEDLINE=20483645; PubMed=11027606; DOI=10.1006/bbrc.2000.3586; McKenzle E., Tyson K., Stamps A., Smith P., Turner P., Barry R. Hircock M., Patel S., Barry E., Stubberfield C., Terrett J., P. "Cloning and expression profiling of Hpa2, a novel mammalian heparanase family member.";
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PPACLAPGALYLALLHLSLSSQAGDRRPLPVDRAAGLKEKTLILLDVSTKNPVRTVNEN
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                                                                                                    Query Match
Best Local S
Matches 184
                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=p50; TISSUE=Posterior silkgland;
Koike Y., Mita K., Suzuki M.G., Maeda S., Al
Koike Y., Mita K., Suzuki M.G., Maeda S., Al
GeJong P.J., Shimada T.;
"Genomic sequence of a 320 kb segment of the
mori containing a kettin ortholog.";
Mol. Genet. Genomics 269:117-149 (2003).
EMBL; AB079860; BAB85191.1; -.
EMBL; AB079860; BAB85191.1; -.
EMBL; AB09307; BAC10612.1; -.
EMBL; AB090307; BAC10612.1; -.
EMBL; AB09362; Glyco hydro 79n; I
InterPro; IPR0362; Glyco hydro 79n; I
SEQUENCE 515 AA; 59769 MW; FB8100ABE6ED;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q8T108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2002 (TrEMBLrel.
05-JUL-2004 (TrEMBLrel.
Heparanase-like protein.
Name=Bmhepa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; BomBombycidae; Bombyx.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=7091;
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                                                                                                      184;
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                                                46
                                                                                                                               Similarity
                                   QEPLHLVSPSFLSVTIDANLATDPRFLILLGSPKLRTLARGLSPAYLRFGGTKTDFLIFD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAPLLSDTFAAGFMWLDKLGLSARMGIEVVMRQVFFGAGNYHLVDENFDPLPDYWLSLLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FLSVTIDANLATDPRFLILLGSPKLRTLARGLSPAYLRFGGTKTDFLIF----DPKKEST 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KYLRLPYPPSNKQVDKYLLRPLGPHGLLSKSVQLNGLTLKMVDDQTLPPLMEKPLRPGSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DAVTWQHCYIDGRVVKVMDFLKTRLLDTLSDQIRKIQKVVNTYTPGKKIWLEGVVTTSAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DSVTWHHYYLNGRTATREDFLNPDVLDIFISSVQKVFQVVESTRPGKKVWLGETSSAYGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MHGRAVNGSQLGKDYIQLKSLLQPIRIYSRASLYGPNIGRPRKNVIALLDGFMKVAGSTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KADIFINGSQLGEDFIQLHKLLRK-STFKNAKLYGPDVGQPRRKTAKMLKSFLKAGGEVI
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QEDIKLISEDFLSFGID-TIEIENYNRINYSDTRLRELAAALSPARLRLGGTMSERLIF-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KKIKLAGTLRDKLVHQYLLQPYGQEGLKSKSVQLNGQPLVMVDDGTLPELKPRPLRAGRT 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KRLIGPKVLAVHVAGLQRKPRPGRVIRDKLRIYAHCTNHHNHNYVRGSITLFIINLHRSR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Silk moth).
                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                    24.6%; Score 699; DB 2; L 35.2%; Pred. No. 3.1e-44; tive 82; Mismatches 182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21,
21,
27,
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Last annotation update)
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                                                                                                      indels
                                                                                                                                                                                                                                                                                                                                                                                             of Bombyx
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                                                                                                      74;
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                                                                                                      Gaps
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PLGPLSPGAL------PRPA-----QAQDVVDLDFFTQEPLHLVSPS

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Q8WWQ1
ID Q8WWQ
AC Q8WWQ
DT 01-MA
DT 01-JU
DE Hepar
OS Homo
OC Eukar
OS Homo
OC Mamma
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RA Legou
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                                      Query Match
Best Local S
Matches 223
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Q8WWQ1;
01-MAR-2002
01-MAR-2002
                                                                                                                                                                                                                                                                                                        Heparanase 3. Homo sapiens
                                                                                          Pessegue Safontas B.J.O.P.S.;
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ
EMBL; AJ299720; CAC82492.1; -
Pfam; PF03662; Glyco hydro 79n; 1.
SEQUENCE 548 AA; 61771 MW; B8986303FC73A60
                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                     01-JUN-2003
                                                                                                                                                                                                    Legoux P., Legoux R.,
Submitted (JAN-2002) 1
                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                           TISSUE=Prostate;
                                                                                                                                                             ISSUE=Prostate;
                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           556
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             8
                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FLSVTIDANLATDPRFLILLGSPKLRTLARGLSPAYLRFGGTKTDFLIF----DPKKEST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DITLYAINLHNVTKYLRIPYPFSNKQVDKYLLRPLGPHGLLSKSVQLNGLTLKMVDDQTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MLKSFLKAGGEVIDSVTWHHYYLNGRTATREDFLNPDVLDIFISSVQKVFQVVESTRPGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SWELGNEPNNYRTMHGRAVNGSQLGKDYIQLKSLLQPIRIYSRASLYGPNIGRPRKNVIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SWELGNEFNSFLKKADIFINGSQLGEDFIQLHKLLRK-STFKNAKLYGFDVGQPRRKTAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYSNLILTARSLDKLYNSÅDCSGLHLIFALNÅLRRNPNNSWNSSSALSLLKYSASKKYNI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           PELKPRPLRAGRTLVIPPVTMGFFVVKNVNALAC 589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PPLMEKPLRPGSSLGLPAFSYSFFVIRNAKVAAC 542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FNPLPDYWLSLLYKRLIGPKVLAVHVAGLQRKPRPGRVIRDKLRIYAHCTNHHNHNYVRG
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                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                            (Human)
                                                                                                                                                                                                                                                                                   Primates;
                                                                                                                                                                                                                                                                                              Chordata;
                                                   35.6%;
                                                                                                                                                                                                    to the EMBL/GenBank/DDBJ
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20,
24,
=
                                        ; 08
                                      Score 1011.5;
Pred. No. 7.1e.
80; Mismatches
                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                                                                                             B8986303FC73A60A
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                                                                                                                                                                                                                                                                                                                                                                                          548
                                                  .5; DB 2;
7.1e-68;
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                                      180;
           ----PRPA-----QAQDVVDLDF
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                                                                                             CRC64;
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                                                                 Length
                                                                  548;
                                        53;
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CO Homo
OC Eukar
OS Homo
OC Eukar
CO MAMMA
DT HEPAR
CO MCAIN
RN | [1] ---
RN | [1] ---
RN Hiroc
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RT HOFT
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RT HOFT
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RP SEQUI
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                                                                                                         Query Match
Best Local S
Matches 216
                                                                                                                                                                       SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MCKENZIE E.A., Tyson K., Stamps A.;

MCKENZIE E.A., Tyson K. the EMBL/GenBar

Submitted (JUN-2000) to the EMBL/GenBar

EMBL; AF282886; AAG23422.1; -

InterPro; IPR005199; Glyco hydro 79N.

Pfam; PF03662; Glyco hydro 79n; I.

SEQUENCE 534 AA; 60063 MW; C3DE5E9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2001 (TYEMBLIEL 16, Created)
01-MAR-2001 (TYEMBLIEL 16, Last sequence update)
01-MAR-2004 (TYEMBLIEL 26, Last annotation update)
Heparanase-like protein HPA2b.
                                                                                                                                                                                                                                                                                                                 "Cloning and expression profiling of Hpa2, a novel mammalian heparanase family member."; Biochem. Biophys. Res. Commun. 276:1170-1177(2000).
                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=20483645; PubMed=11027606; DOI=10.1006/bbrc.2000.3586; MCKenzie E., Tyson K., Stamps A., Smith P., Turner P., Barry R., Stubberfield C., Terrett J., F
                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9HB38;
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9HB38
                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
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                                                                                                                          Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EQL-LLREHYQKKFKNSTYSRSSVDVLYTFANCSGLDLIFGLNALLRTADLQWNSSNAQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STKNPVRTVNENFLSLQLDPSIIHD-GWLDFLSSKRLVTLARGLSPAFLRFGGKRTDFLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FTQEPLHLVSDSFLSVTIDANLATDPRFLIILGSPKLRTLARGLSPAYLRFGGTKTDFLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AFPEAMLSSNSRPPACLAPGALYLALLLHLSLSSQAGDRRPLPVDRAAGLKEKTLILLDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VFQVVESTRPGKKVWLGETSSAYGGGAPLLSDTFAAGFMWLDKLGLSARMGIEVVMRQVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PNIGRPRKNVIALLDGEMKVAGSTVDAVTWQHCYIDGRVVKVMDFLKTRLLDTLSDQIRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LLDYCSSKGYNISWELGNEPNSFLKKADIFINGSOLGEDFIOLHKLLRK-STFKNAKLYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F----DPKKESTFEERSYWQSQVNQDI-----CKYGSIPPDVEEKLRLEWPYQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTNHHNHNYVRGSITLFIINLHRSRKKIKLAGTLRDKLVHQYLLQPYGQEGLKSKT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FGAGNYHLVDENFDPLPDYWLSLLFKKLVGTKVLMASVQGSKRR-------KLRVYLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IQKVVNTYTPGKKIWLEGVVTTSAGGTNNLSDSYAAGFLWLNTLGMLANQGIDVVIRHSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PDVGQPRRKTAKMLKSFLKAGGEVIDSVTWHHYYLNGRTATREDFLNPDVLDIFISSVQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LLKYSASKKYNISWELGNEPNNYRTMHGRAVNGSQLGKDYIQLKSLLQPIRIYSRASLYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FONLRNPAKSRGGPGPDYYLKNYEDDIVRSDVALDKOKGCKIAQ-HPDVMLELQREKAAQ
   FLSVTIDANLATDPRFLILLGSPKLRTLARGLSPAYLRFGGTKTDFLIF---
                                    PPACLAPGALYLALLHLSLSSQAGDRRPLPVDRAAGLKEKTLILLDVSTKNPVRTVNEN
                                                                       PLGPLSPGAL----
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                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                        32.8%;
                                                                                                                                                                                                                                                K., Stamps A.;
to the EMBL/GenBank/DDBJ
                                                                                                         Score 932.5; DB 2
Pred. No. 6.6e-62;
9; Mismatches 168
                                                                                                                                                                              C3DE5E900CB338C4 CRC64;
                                                      -PRPA------QAQDVVDLDFFTQEPLHLVSPS
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AC Q9HB
AC Q9HB
DT 01-M
DT 01-M
DT 01-J
DE Hepa
OS Homo
OC Euka
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                              Query Match
Best Local S
Matches 249
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                                                                                                                 McKenzie E.A., Tyson K., Stamps A.;
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ
EMBL; AF2828897; AA623423 1; -
GO; GO:0005622; C:intracellular; TAS.
GO; GO:0030305; F:heparanase activity; TAS.
InterPro; IPR005199; Glyco_hydro_79N.
Pfam; PF03662; Glyco_hydro_79n; 1.
SEQUENCE 592 AA; 66580 MW; 95C384AD9A74259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9НВ37
Q9НВ37;
                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

MEDLINB=20483645; PubMed=11027606; DOI=10.1006/bbrc.2000.3586;

MCKCHIZLE E., Tyson K., Stamps A., Smith P., Turner P., Barry R.

Hircock M., Patel S., Barry E., Stubberfield C., Terrett J., P.

"Cloning and expression profiling of Hpa2, a novel mammalian heparanase family member.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Heparanase-like protein HPA2c.
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                        Biochem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
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                                                        Similarity
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                                                                                                                                                                                                                                                                                                                                                        Biophys.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EVQLNGRLLQMVDDETLPALHEMALAPGSTLGLPAFSYGFYVIRNAKAIACI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     L-RKSTFKNAKLYGPDVGQPRRKTAKMLKSFLKAGGEVIDSVTWHYYLNGRTATREDFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RTADLQWNSSNAQLLLDYCSSKGYNISWELGNEPNSFLKKADIFINGSQLGEDFIQLHKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FAVVPKLLLTQWPLQEKLLLAEHSWKKHKNTTITRSTLDILHTFASSSGFRLVFGLNALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PPDVEEKLRLEWPYQEQLLLREHYQKKFKNSTYSRSSVDVLYTFANCSGLDLIFGLNALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALLRHPKLHTLASGLSPGFLRFGGTSTDFLIFNPNKDSTWEEKVLSEFQA-KDVCEAWPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RRAGLOWDSSNAKQLLGYCAQRSYNISWELGNEPNSFRKKSGICIDGFQLGRDFVHLRQL
                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                        Res. Commun.
                                                    40.5%;
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                              Score 1150.5; DB 2;
Pred. No. 2.3e-78;
3; Mismatches 189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                        276:1170-1177(2000)
                                                                                                                           95C384AD9A74258E CRC64;
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Query Match
Best Local Similarity
Matches 248; Conserv
                                                                                     Pessegue Safontas B.J.O.P.S.;
Submitted (SEP-2000) to the E
EMBL; AJZ99719; CAC62491.1; -
Genew; HGNC:18374; HPSE2.
Pfam; PF03662; Glyco hydro 79
SEQUENCE 592 AA; 66520 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Heparanase 2.
Homo sapiens (Human).
Eukaryota; Metazoa; Ch
Mammalia; Eutheria; Pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q8WWQ2;
01-MAR-2002 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                 Legoux P.,
Submitted
                                                                                                                                                                                                                               TISSUE=Prostate;
                                                                                                                                                                                                                                                                                                                                            TISSUE=Prostate;
                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                 (JAN-2002)
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                                                                                       Glyco hydro 79n;
AA; 66520 MW; 9
                                                                                                                                                                                                                                                                                                                                                                                                                                    Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
                     40.2%; Score 1142.5; DB 2; 43.2%; Pred. No. 9.4e-78;
                                                                                                                                                                                                                                                                                               to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20,
                                                                                                                                                                                 EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation updat
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                                                                                                                                                                                    databases
                                                                                                                                                                                                                                                                                                 databases.
                                                                                          CRC64;
                                          Length 592;
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Conservative

83;

Mismatches

53;

Gaps

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InterPro; IPR005199; Glyco_hydro_
Pfam; PF03662; Glyco_hydro_79n; 1
SEQUENCE 536 AA; 60479 MW; C4
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Hulett M.D., Wang J., Hornby
Parish C.R.;
Submitted (MAR-2001) to the
                                                                                                                 SEQUENCE FROM N.A.

MEDLINE=22194309; PubMed=12077130; DOI=10.1074/jbc.M203282200;

MEDLINE=22194309; PubMed=12077130; DOI=10.1074/jbc.M203282200;

Podyma-Inoue K.A., Yokote H., Sakaguchi K., Ikuta M., Yanagishita Podyma-Inoue K.A., Yokote H., Sakaguchi K., Ikuta M., Yanagishita Podyma-Inoue K.A., Yokote H., Sakaguchi K., Ikuta M., Yanagishita Podyma-Inoue K.A., Yanagishita Podyma-Inoue K.A., Yanagishita Podyma-Inoue K.A., Yokote H., Sakaguchi K., Ikuta M., Yanagishita Podyma-Inoue K.A., Yokote H., Sakaguchi K., Ikuta M., Yanagishita Podyma-Inoue K.A., Yokote H., Sakaguchi K., Ikuta M., Yanagishita Podyma-Inoue K.A., Yokote H., Sakaguchi K., Ikuta M., Yanagishita Podyma-Inoue K.A., Yokote H., Sakaguchi K., Ikuta M., Yanagishita Podyma-Inoue K.A., Yokote H., Sakaguchi K., Ikuta M., Yanagishita Podyma-Inoue K.A., Yokote H., Sakaguchi K., Ikuta M., Yanagishita Podyma-Inoue K.A., Yokote H., Sakaguchi K., Ikuta M., Yanagishita Podyma-Inoue K.A., Yokote H., Sakaguchi K., Ikuta M., Yanagishita Podyma-Inoue K.A., Yokote H., Sakaguchi K., Ikuta M., Yanagishita Podyma-Inoue K.A., Yokote H., Sakaguchi K., Ikuta M., Yanagishita Podyma-Inoue K.A., Yokote H., Sakaguchi K., Ikuta M., Yanagishita Podyma-Inoue K.A., Yokote H., Yanagishita Podyma-Inoue K.A., Yanagishita Podyma-Inoue K.A., Yokote Podyma-Inoue Podyma-Ino
                                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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01-JUN-2002
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   SEQUENCE FROM N.A. Podyma K.A., Yokote Submitted (SEP-1999)
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76.3%;
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13,
21,
      Sakaguchi K., Ikuta M. the EMBL/GenBank/DDBJ
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Sciurognathi; Muridae;
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01-DEC-2001
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SEQUENCE FROM N.A.

MEDLINE-21369959; PubMed-11387326; DOI=10.1074/jbc.M102462200;

Goldshmidt O., Zcharia E., Aingorn H., Guatta-Rangini Z., Atzm

Goldshmidt D., Zcharia E., Vlodavsky I.;

Michal I., Pecker I., Mitrani E., Vlodavsky I.;

"Expression pattern and secretion of human and chicken heparan

determined by their signal peptide sequence.";

J. Biol. Chem. 276:29178-29187(2001).

EMBL; AV037007; AAK82648-1; -.

Pfam; PF03662; Glyco hydro_79n; 1.

SEQUENCE 523 AA; 58386 MW; BEB0B7B18C9BF881 CRC64;
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Gallus gallus (Chicken).

Gallus gallus (Chicken).
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PF03662; Glyco_hydro_79n; I.
NCE 536 AA; 60568 MW; 6208B1FD9EE28421
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Eukaryota; Metazoa; C
Mammalia; Eutheria; R
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Q6YGZ1;
05-JUL-2004
05-JUL-2004
05-JUL-2004
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GO; GO:0005578; C:extracellular matrix
InterPro; IPR005199; Glyco_hydro_79N.
Pfam; PF03662; Glyco_hydro_79n; I.
SEQUENCE 535 AA; G0065 MW; 6E73A830
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                                                                                                                                    VQLNGQILKMVDEQTLPALTEKPLPAGSALSLPAFSYGFFVIRNAKIAACI
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(TrEMBLrel.
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                                                                                   PRELIMINARY;
   Chordata;
Rodentia;
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Pred. No. 2.1e
50; Mismatches
                                        Created)
Last sequence update)
Last annotation update)
  Craniata; Vertebrata; Sciurognathi; Muridae;
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hizaki Y.;
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Best Local S
Matches 408
  Heparanase.

Name=Hspe;
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; C
Mammalia; Eutheria; Rodentia; S
NCBI TaxID=10116;
[1]
                                                                                                                                            Q71RP1;
Q71RP1;
Q5-JUL-2004
05-JUL-2004
05-JUL-2004
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SEQUENCE
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Submitted (SEP-2002) to the EMBL/GenBan

EMBL; AY151051; AAN41036.1; -.

GO; GO:0005578; C:extracellular matrix

InterPro; IPR005199; Glyco.hydro.79N.

Pfam; PF03662; Glyco.hydro.79n; I.

SEQUENCE 535 AA; 59992 MW; 3748AEB3
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SEQUENCE FROM N.A.

MEDLINE=22841152; PubMed=12837765; DOI=10.1074/jbc.M300925200;

Gong F., Jemth P., Galvis M.L.E., Vlodavsky I., Horner A., Lin
Li J.P.;

"Processing of macromolecular heparin by heparanase.";

J. Biol. Chem. 278:35152-35158(2003).
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76.8%; Pred. No. 1.26
vative 49; Mismatches
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01-OCT-2000
01-JUN-2001
01-JUN-2002
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EMBL; AF281160; AAF87301.2; -
Interpro; IPR005199; Glyco hydro 79N.
Pfam; PF03662; Glyco hydro 79n; I.
SEQUENCE 545 AA; 61076 MW; FAC4BDFFD8
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Mammalia; Eutheria;
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C STRAIN=CS7BL/60; TISSUE=Thymus;

C STRAIN=CS7BL/60; TISSUE=Thymus;

X MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

X MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

X MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

X MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

A Sumin N., Ishii Y., Nakamura S., Hazama M., Nishine T., Itoh M.,

A Sumin N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,

A Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,

A Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,

A Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,

A Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,

A Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

T "RIKEN integrated sequence analysis (RISA) system-384-format

sequencing pipeline with 384 multicapillary sequencer.";

L Genome Res. 10:1757-1771(2000).
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01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Heparanase (Mus musculus 0 day neonate thymus cDNA, RIK
enriched library, clone:A430101M04 product:heparanase,
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STRAIN=C57BL/6J; TISSUE=Thymus;

MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.14510;

Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibat Konno H., Okazaki Y., Muramateu M., Hayashizaki Y.;

"Normalization and subtraction of cap-trapper-selected prepare full-length cDNA libraries for rapid discovery Genome Res. 10:1617-1630(2000).
SEQUENCE FROM N.A.

STRAIN-(57BL/6J; TISSUE=Thymus;
STRAIN-(57BL/6J; TISSUE=Thymus;
Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carni Adachi J., Aizawa K., Akimura T., Hara A., Hashizume W., Fukuda S., Furuno M., Hanagaki T., Hara A., Hirozane Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=C57BL/6J; TISSUE=Thymus; MEDLINE=99279253; PubMed=10349636; Carninci P., Hayashizaki Y.; "High-efficiency full-length cDNA c Meth. Enzymol. 303:19-44(1999).
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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STRAIN=C57BL/6J; TISSUE=Thymus;
The FANTOM Consortium,
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STRAIN=C57BL/6J; TISSUE=Thymus;
MEDLINE=21085660; PubMed=11217851;
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Sciurognathi;
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Kouda M., F
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Murinae; Mus
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Ishai-Michaeli R., Bitan M., Pappo O., Peretz T., Michal I.

Spector L., Pecker I.;

Spector L., Pecker I.;

Submitted (ApR-1999) to the EMBL/GenBank/DDBJ databases.

EMBL, AF165154; AAD45379.1; -.

EMBL; AF152376; AAD45679.1; -.

EMBL; AF152376; AAD45679.1; -.

REMBL; AF152310; AAD54941.1; -.

REMBL; BC051321; AAH51321.1; -.

REMBL; BC051321; AAH51321.1; -.

REMBL; AF144225; AAD41342.1; -.

REMBL; AF144225; AAD41342.1; -.

REMBL; AF144225; AAD41342.1; -.

REMBL; AF14425; AAD41342.1; -.

REMBL; AF14425; AAD5491.1; -.

REMBL; AF14425; AAD5491.1; -.

REMBL; AF14425; AAD51321.1; -.

REMBL; AF14425; AAD51321.1; -.

REMBL; AF14425; AAD51321.1; -.

REMBL; AF14425; AAD51321.1; -.

REMBL; AF14425; AAD451321.1; -.

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REMBL; AF1551321.1; -.

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Matches 543; Conservative (
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TISSUE=Pancreas;
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"Generation and initial analysis of more than 15,000 full-length and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (APR-2003)
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Pred. No. 1.6e-206;
; Mismatches 0;
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Q9UL39; O1-MAY-2000 (TrEMBLrel. 13, Created)
O1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
O1-UN-2002 (TrEMBLrel. 21, Last annotation update)
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EMBL; AF084467; AAD54516.1; -.

Genew; HGNC:5164; BAD54516.1; -.

Genew; InterPro; IPR005199; Glyco hydro 7

Pfam; PF03662; Glyco hydro 79n; I.

SEQUENCE 545 AA; 61417 MW; 67B
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Butheria; Primates; Catarrhini; Hominidae;
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MEDLINE=20229546; PubMed=10764835; DOI=10.1093/glycob/10.5.
Dempsey L.A., Plummer T.B., Coombes S.L., Platt J.L.;
"Heparanase expression in invasive trophoblasts and acute v
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99.6%; Pred. No. 6.3e-205;
tive 0; Mismatches 0;
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1 MLLRSKPALPPPLMLLLLGP.....LPAFSYSFFVIRNAKVAACI 543
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched:

Total number of hits satisfying chosen parameters: 1612378 seqs, 512079187 residues

1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Query Query Query Query Ratch Length DB ID Description 2841 2993 2845 29139 2945 2754 2754 2754 2754 2754 2754 2755 2754 2755 2754 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755 2755	3302276 330276 330276 330276	U U U U U U	Regult No.
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	O7irp1 rattus n O9qrf8 rattus n O9hb37 homo sap O8hwq2 homo sap O8hw31 homo sap O9hb39 homo sap O9hb39 homo sap O9ff10 arabidop O9ff10 arabidop O9ff10 arabidop O9ff10 arabidop O9f1c8 scutella O70yj3 hordeum O9fzp1 arabidop O9f1k8 arabidop O9f1k8 arabidop O8f1608 arabidop O8f1608 arabidop O8f1608 arabidop O8f1608 arabidop O8f1608 arabidop O8f1609 burkhold O9sh601 thermopl O9sh601 thermopl	homo homo bos mus	

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670	617	617	2319	732	617	1829	617	398	398	1169	390	617	408
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Q9M090	Q98VH5	040991	Q96U00	Q7MSD4	Q83647	Q9KH44	Q83295	Q8F410	Q72RP7	Q869K5	OSTPH7	040996	Q9HEZ2
Q9m090	Q98vh5	040991	Q96u00	Q7msd4					Q72rp7	Q869k5	Q8tph7	040996	Q9hez2
arabidopsi	measles vir	measles vir	neurospora	wolinella s	measles vii	pantoea ago		leptospira		dictyostel:		measles vi	phanerochae

ALIGNMENTS

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elton E., Ketteman M., Madan A., Rodrigues S., Madan A., Young A.C., Shevchenko Y., Bouffard	, Worley K.C., Hale S., Garcia A.M., Gay L.J., Huly K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,	stein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.	, Marusina K., Farmer A.A., Rubin G.M., Hong L.,	R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.	ollins F.S., Wagner L., Shenmen C.M., Schuler eeberg B., Buetow K.H., Schaefer C.F., Bhat N	Feingold E.A., Grouse L.H., Derge J.G.,	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;	SEQUENCE FROM N.A.		expression."; J. Biol. Chem. 274:24153-24160(1999).	nase. Purifi	jima M.	SEQUENCE FROM N.A. MEDLINE=99377052: PubMed=10446189; DOI=10.1074/jbc.274.34.24153;		Biophys. Res. Commun. 261:183-187(1999).	ng and functional expression	Seddon A.P. Giorgio N.A. Bohlen P.:	E=99335379; PubMed=10405343; DOI=10.1006/bbrc.1999.09		SEQUENCE FROM N.A.	NAT. MEG. 5:803-809(1999).	sion and metastasis.";		rreeman C., Hamdori	E=99321249; PubMed=10395326;	lacenta;	SEQUENCE FROM N.A.	I_TaxID=9606;	Butheria; Primates; Catarrhini; Hominidae;	Chordata: Craniata: Vertebrata: Euteleostomi	=HPA; Syn	(TIBMBLIET.	1999 (TrEMBLrel. 12, Last sequence update)	(TrEMBLrel. 12, Created)	09Y251 PRELIMINARY; PRT; 543 AA.	LT 1

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A; Gene: ADE1; SPDB: SPBC405.01

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A;Map position: 2
C;Superfamily: Saccharomyces cerevisiae ADE5 multifunctional protein; phosphoribosylamin C;Keywords: cyclo-ligase; purine nucleotide biosynthesis C;Keywords: cyclo-ligase; purine nucleotide biosynthesis F;5-425/Domain: phosphoribosylamine-glycine ligase homology <PGL> F;439-767/Domain: phosphoribosylformylglycinamidine cyclo-ligase homology <PFCL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-432 <AQF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus A;Reference number: A70300; MUID:98196666; PMID:9537320 A;Accession: F70411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 392, 353-358, 1998
A;Title: The complete gend
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  adenylosuccinate synthetase - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
C;Accession: F70411
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A;Experimental source: strain VF5
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                                   166 SRSSVDVLYTFANCSGLDLIFGLNALLRTADL----QWNSSNAQLLLDYCSSKGYNISWE 221
                                                                                      155
                                                                                                                                                                           110 H------KLLDSLFEKKKGIGTTLRGIGPAYMFKYG--RKGIRISDLKDEKRF
                                                                                                                                                                                                                                                                 51 ILHLLPTGILHEHVKGVIAQGM-VVDLEVLHKEVKNLEEKGIYVKERLFISDRAHLVMPY 109
                                                                                                                                                                                                                       56 FLSVTIDANLATDPRFLILLGSPK--LRTLARGLSPAYL-RFGGTKTDFLIFDPKKESTF 112
                                                                                                                                                                                                                                                                                                              15 LLLLGPLGPLSPGALPRPAQAQDVVDLD-------FFTQEPLHLVSPS
                                                                                                                                                                                                                                                                                                                                                           ; 96
                                                                                                                                                                                                                                                                                                                                                                                h 3.7%; Score 104; DB Similarity 23.9%; Pred. No. 6.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YLRLPYPFSNKQVDKYLLRPLGPHGLLSKSVQLNGLTL--KMVD----DQTLPPLMEKPL 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGWNDPLLVSATDGVGSKLLIALSLNKHDTVGIDLVAMNV-----NDLVVQGAEPLIFL 537
                                                                                                                              EERSYWQSQVNQDICKYGSIPPDVEEK-----LRLEWPYQEQLLLREHYQKKFKNSTY 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RLGDSLLIPTRIY 663
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HHALNPKRKTREILTYENSGVSVDNGNEFVQRIKDLVKSTRRPGADADIGGFGGIFDLKQ 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DYFATGSLDLKVSTSFVEGVVKGCKQAGCALVGGETSEMPGLYHDGHYDANGTSVGAVSR
----VDLLRFFNTQKGSVLFEGAQGTLLDVDMGTYPYVTSSNASAL---
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                                                                                                                                                                                                                                                                                                                                                             39; Mismatches 128; Indels 138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 104.5; I
Pred. No. 15;
36; Mismatches
                                                                                         --NICEKVFCEKFDLDINQIYEEQL----RYFEEFKENV- 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GLASDGVHSNGYSLVRKIVEYSDLEYTSVCPWDKNV
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  --GLSNG 246
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В	Qy	Дb	δ	ģ	Qγ
344	314	296	266	247	222
344 YELDGEVIDYFPASYSELIRVKPVYKTLKGWKKSTKGA 381	314DVLDIFISSVQKVFQVVESTRPGKKVWLGETSSA 347	G	266 PDVGQPRRKTAKMLKSFLKAGGEVIDSVTWHHYYLNGRTATREDELNP 313	247 TGMPPKYFSDAFFLGVAKAYTTRVGEGPFPTELKGEEGEKLRELGGEYG 295	222 LGNEPNSFLKKADIFING
		43	ü	95	9

Search completed: March 23, 2005, 11:31:39 Job time: 30 secs

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RESULT 13
T38446
                                                                                                                                                                                                                                                        microtubule-associated protein ssm4 - fission yeast (Schizosaccharomyces pon C;Species: Schizosaccharomyces pombe C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004 C;Accession: T38446; T00012
R;McDougall, R.; Wood, V.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, December 1997
                                              A;Title: Microtubule-associated coiled-coil protein Ssm4 is A;Reference number: Z14042; MUID:97311255; PMID:9167972 A;Accession: T00012
                                                                                                   A;Cross-references: UNIPROT:042667; EMBL:AL009227; PIDN:CAA15832.1; A;Experimental source: strain 972h; cosmid c27D7 R;Yamashita, A; Watanabe, Y, Yamamotto, M. Genes to Cells 2, 155-166, 1997
                                                                                                                                                                                                     A;Reference number: Z21793
A;Accession: T38446
A;Status: preliminary; translated from
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A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-670 <YAM>
                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-670 < MCD>
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                                                                                                                                                                                                                                                                                                                                                                                                                                           QADKGVYISLXMPWGD----SSTISYNG 595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NFRDAGVSVYLNYTRHTYWDRDEQTNYNVML---SHYFNLGSIRNMSISMTGYRYEYDN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LSYSKDEDELNSRVTFAG---YRFSEENEMTMSEY-LDASDSEMVRTGNDKEMYTATYNQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYSRSSVDVLYTFANCSGLDLIFGL-NALLRTADLQWNSSN-----AQLLLDYC----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QVDK----YLLRPLGPHGLLSKSVQLNG 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KRRKLRVYLHCTNTDNPRYKEGDLTLYAINLHNVTKYLRL------PYPFSNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MGI-----EVVMRQVFFGAGNYHLVDENFDPLPDYWLSLLFKKLVGT----KVLMASVQGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SLYGGA---LADEHYQSAALGVGRDLSVFGAVAFDITHSHTRLDKETAYGKGSLDGNSFR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----GIDIK---ADLSQSALVISLPQAYLEYTDINWDPPSRWDDGISGLIADYSITAQT 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EEYDIYWYASENDASKTYACLTPELVAQFGLKEDVAKNLQWIHDGKCLKPGQLE-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MSGSYVNAWAENEIQFDSRFLELKGDTKI-DLKRFSSQGYVEPG--KYNLQVQLNKQPLT
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ilarity 20.5%;
Conservative 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64;
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Pred. No. 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches 201;
                                                                                                                                                                                                          GB/EMBL/DDB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 879;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels 234;
                                                                                  involved
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                                                                                                                                                       GSPDB:GN00066;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -GLSAR
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                                                                                  meiotic
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A;Cross-references: EMBL:AB000269; C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                   Similarity
 SNNSSVDGVKTRR
                        VLMASVQGSKRRK
                                                  -LVKIPKNPFSEKLTISNVNRYLNIVPGSLDLQFSLTNENF----VHWNSTVYQELLNLK 395
                                                                       GFMWLDKLGLSARMGIEVVMRQVFFGAGN----YHLVDENFDPLPDYWLSLLFKKLVGTK
                                                                                                       PKSQDNWTTQVTPSSLLGVSEVSKVLQL-----KQVQVDITE--
                                                                                                                              ATREDFLNPDVLD---IFISSVQKVFQVVESTRPGKKVWLGETSSAYGGGAPLLSDTFAA
                                                                                                                                                                                                                                                                                       RSSVDVLYTFANCSGLD-LIFGLNALLRTADLQWNSSNAQLL-LDYCSSKGYNISWELGN
                                                                                                                                                                                                                                                                                                                   KRPSVVKSR----KKGSENISNFMEKTKAIKQKSRREPSKFERSLARPLCITPIDSSTPT
                                                                                                                                                                                                                                                                                                                                            KKESTFEERSYWQSQVNQDICKYGSIPPDVEEKLRLEWPYQEQLLLREHYQKKFKNSTYS
                                                                                                                                                                                  FKNAKLYGPDVGQPRR-KTAKMLKSFLKAGGEV-----IDSVTWHHYYLNGRT
                                                                                                                                                                                                            VLQECEKKFTPHSKGSYLKENLKSELRKGRLDELMCENTALKEKIDKLNKELEKVEPQLT
                                                                                                                                                                                                                                                                 KTA--TFYTSSTTENLDELNFSTEELSSFDTTLLNSDTSKLSGLDDSSFMEEEFVWQVDN
                                                                                                                                                        FLRSK---NSIEKPRNFRREKFLKKFLAMQKEIKYLRKRKLQIRKIPNYKYSDRSLNSKT
                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                      -EPNSFLKK--
                                                                                                                                                                                                                                                                                                                                                                                   3.7%;
 408
                        430
                                                                                                                                                                                                                                                                                                                                                                        58;
                                                                                                                                                                                                                                                                                                                                                                                Score 105; I
Pred. No. 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                NID:g3341860; PIDN:BAA31857.1; PID:g3341861
                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                     ---ADIFINGSQLGEDYIQLHKLLRK----ST
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                                                                                                                                                                                                                                                                                                                                                                        149;
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                                                                                                                                                                                                                                                                                                                                                                      86;
                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                            417
                                                                                                                               361
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                                                                                                       340
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S00652 RESULT

phosphoribosylamine-glycine ligase (EC 6.3.4.13) - fission yeast (Schizosaccharomyces pon N;Alternate names: AIRSase; aminoimidazole ribotide synthetase; GARSase; glycinamide ribotic N;Contains: phosphoribosylamine-glycine ligase (EC 6.3.4.13); phosphoribosylformylglycine C;Species: Schizosaccharomyces pombe C;ClDate: 07-Sep-1990 #sequence revision 28-Oct-1994 #text_change 09-Jul-2004 C;Accession: S00652; T40496; T40422 R;McKenzie, R.; Schuchert, P.; Kilbey, B. Curr. Genet. 12, 591-597, 1987 A;Title: Sequence of the bifunctional adel gene in the purine biosynthetic pathway of the A;Reference number: S00652; MUID:89003164; PMID:3502942 A;Accession: S00652

A;Molecule type: DNA
A;Residues: 1-788 «MC>
A;Residues: 1-788 «MC>
A;Cross-references: UNIPROT:P20772; EMBL:X06601; NID:g4903; PIDN:CAA29820.1; PID:g4904
A;Cross-veferences: UNIPROT:P20772; EMBL:X06601; NID:g4903; PIDN:CAA29820.1; PID:g4904
A;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Lauber, J.; Hilbert, H.; Duesterhoeft, A.
submitted to the EMBL Data Library, February 1998
A;Reference number: Z21910

A; Reference number: A; Accession: T40496

A;Status: preliminary; translated from GB/EMBL/DDBJ

A; Molecule type: DNA A; Residues: 1-788 < WOO>

A;Cross-references: EMBL:AL021730; PIDN:CAA16823.1; GSPDB:GN00067; SPDB:SPBC4C3.02c

B.G.

A;Experimental source: strain 972h-; cosmid c4C3 R;Seeger, K.; Harris, D.; Wood, V.; Rajandream, I submitted to the EMBL Data Library, March 1999 A;Reference number: Z21928 A;Accession: T40422 м.а.; Barrell,

A; Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA A;Residues: 604-788 <SEE> A;Cross-references: EMBL:AL035655; PIDN:CAB38600.1; GSPDB:GN00067; SPDB:SPBC405.01 A;Experimental source: strain 972h-; cosmid c405

rimental source: strain O157:H7, substrain tics: : Z3600	: : : :::: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
A;Status: preliminary A;Molecule type: DNA A;Residues: 1-879 <sto> A;Cross-references: UNIPROT:Q8XCP4; GB:AE005174; NID:g12516702; PIDN:AAG57466.1; GSPDB:GN</sto>	208 245
Nature 407, 523-533, 2001 A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7. A;Reference number: A85480; MUID:21074935; PMID:11206551 A;Accession: F85875	Db 151 EFRLISPTREQIDIFAGSTKLDLLASEENIDCIVHLANPRVYTSNVAMGQTLTMLRN 207 Qy 207 LLDYCSSKGYNISWELGNEPNSFLKKADIFINGSQLGE 244
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew, iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,	159 KFKNSTYSRSSYDVLYTFANCSGLDLIFGLNALLRTADLQWNSSNAQL 20
es: Escherichia coli 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004 sion: F85875	Query Match 3.8%; Score 108.5; DB 2; Length 411; Best Local Similarity 21.4%; Pred. No. 2.7; Matches 66; Conservative 55; Mismatches 94; Indels 93; Gaps 17;
RESULT 12 F85875 probable fimbrial usher Z3600 [imported] - Escherichia coli (strain O157:H7, substrain EI	A;Cross-references: UNIPROT:P72895; EMBL:D90901; GB:AB001339; NID:g1651897; PIDN:BAA1691 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
Db 249 SPSP-DAVVGDVRRVREQIEASAFPGLPLYFTEWSTSY 285	A;Accession: 3/4/00 A;Status: preliminary A;Molecule type: DNA A:Beeidung: 1-411 ZVN
Qy 312 NPDVLDIFISSVQKVFQVVE-STRPGKKVWLGETSSAY 348	8. A;Reference number: S74322; MUID:97061201; PMID:8905231
Qy 261 AKLYGPDVGQPRRKTAKMLKSFLKAGGEVIDSVTWHHYYLNGRTATREDFL 311	ura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Y 109-136, 1996 quence analysis of the genome of the unicellular cyanobacter
Db 141 VHHLRARYGVEEVRTWFFEVWNEPNLDGFWEKADQAAYFELYDVTARA 188	Apr-1997 #text_change 09-Jul-2004
310	hypothetical protein slr1617 - Synechocystis sp. (strain PCC 6803) C.Species: Synechocystis sp.
Qy 165 YSRSSVDVLYTFANCSGLDLIFGLNALLRTADLQWNSSNAQLLLD 209	RESULT 10 S74760
Query Match 3.8%; Score 107.5; DB 2; Length 500; Best Local Similarity 25.7%; Pred. No. 4.4; Matches 56; Conservative 35; Mismatches 80; Indels 47; Gaps 15;	Db 576 GVYISLSMEWGDSSTISYNGNYGSGSDSSQVGYFSRVDDAT 616
CC2357	
A;Residues: 1-500 <sto> A;Cross-references: UNIPROT:Q9A5U0; GB:AE005673; NID:g13423886; PIDN:AAK24328.1; GSPDB:GN C;Genetics:</sto>	Qy 427 KRRKLRVYLHCTNTDNPRYKEGDLTLYAINLHNVTK 462 :
A, Status: preliminary A, Molecule type: DNA	Db 460 LSYSKDFDELNSRVTFAGYRFSEENFWTWSEY-LDASDSEMVRTGNDKEMYTATYNQ 515
A;Title: Complete Genome Sequence of Caulobacter crescentus. A;Reference number: A87249; MUID:21173698; PMID:11259647 A.Accession. D87541	ENFDPLPDYWLSLLFKK
B.; Laub, M.T.; DeBoy, K.T.; Dodson, K.J.; Durkin, A.S.; Gwinn, M.L.; Hait, D.R.; Nolone n, J.; Ermolaeva, M.; White, O.; Salabberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001	Qy 346 SAYGGAPLISDTFAAGFWILDKLGSAR 374
ion: D87541 1, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelbe	GQVQEYDINTASMPFLTRPGQVRYKLMMGRPQEWGHHVEGGFFSGGEASWGIANGW
s: Caulobacter cres 20-Apr-2001 #sequen	313 PDVLDIFISSVQKVFQVVESTRPGKKVWLGETS
KESULT 11 D87541 beta-xvlosidase (imported) - Caulobacter crescentus	Db 297 SGVAHTTAKVTVSQLGRVIYETQVPAGPFRIQDLGDSVSGTLHIRIEEQN 346
	Qy 269 GQPRRKTAKMIKSFIKAGGEVIDSVTWHHYYINGRTATREDFIN 312
Db 401 LKSLLHQI 408	Db 243 YYAWRALPSLKAKLGLGEDYLNSDIFDGFNYVGGSISTDDQMLPPNLRGYAPDI 296
Qy 416 TKVLMASV 423	Qy 242LGEDYIQLHKLLRKSTFKNAKLYGPDV 268
Qy 361 AGFMWLDKLGLSARMGIEVVMRQVFFGAGNYHLVDENFDFLPDYWLSLLFKKLVG 415	Qy 212 25KGYNI-SWEL-GNEPNSFLKKADIFINGSQ 241 : : :
	KADLSQSALVISLPQAYLEYTD
QY 305 ATREDFLNPDVLDIFISSVQKVFQVVESTRPGKKVWLGETSSAYGGGAPLLSDTFA 360	Qy 164 TYSRSSVDVLYTFANCSGLDLIFGL-NALLRTADLQWNSSNAQLLLDYC 211

249 SPSP-DAVVGDVRRVREQIEASAFPGLPLYFTEWSTSY 285	Db
312 NPDVLDIFISSVQKVFQVVE-STRPGKKVWLGETSSAY 348	δ
189 IKAIDPSLRVGGPATAGAAWVPEFLAHVKKSGSAVDFVTTHTYGVDGGFLDEKGVQDTKL 248	Дb
261 AKLYGPDVGQPRRKTAKMLKSFLKAGGEVIDSVTWHHYYLNGRTATREDFL 311	γQ
WFFEVWNEPNLDGFW	皮
210 -YCSSKGYNISWELGNEPNSFLKKADIFINGSQLGEDYIQLHKLLRKSTFKN 260	Qγ
81 YDWTKIDQLYDALLAKGIKPFIELGFTPEAMKTSDQTIFYWKGNTSHPKLGPWRDLIDAF 140	Дb
165 YSRSSVDVLYTFANCSGLDLIFGLNALLRTADLQWNSSNAQLLLD 209	8
Query Match 3.8%; Score 107.5; DB 2; Length 500; Best Local Similarity 25.7%; Pred. No. 4.4; Matches 56; Conservative 35; Mismatches 80; Indels 47; Gaps 15;	Quer Best Matc
: 1-50 ference : : 2357	A;Res A;Crc C;Gen A;Gen
A;Accession: D87541 A;Status: preliminary A:Molecule type: DNA	A;Acc A;Sta
enome Sequence of Cauloba A87249; MUID:21173698; F	A;Tit A;Ref
B.; Laub, M.T.; Deboy, K.T.; Dodson, K.J.; Durkin, A.S.; Gwinn, M.D.; Fatt, D.A.; Kolons n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001	n, J. Proc.
T. T. T. W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.: T. T. T. W.C.; Foldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.:	R;Nie
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004	C;Dat
beta-xylosidase [imported] - Caulobacter crescentus	beta-
7 11	RESULT
401 LKSLLHQI 408	DЬ
416 TKVLMASV 423	Qγ
352 IAEMIRDELGSSSMIQQIEVNTEVASIAMNYGRAN-HVLDWEPVIFFE-QG 400	Db
361 AGEMWLDKLGLSARMGIEVVMRQVFFGAGNYHLVDENFDPLPDYWLSLLFKKLVG 415	Ŋ
312NPKLDLLHIDDLISSIVATLKSRFIGNLNIGTGQLSSTLK 351	DЬ
305 ATREDFLNPDVLDIFISSVQKVFQVVESTRPGKKVWLGETSSAYGGGAPLLSDTFA 360	γQ

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A;Cross-retraction: 2R
A;Map position: 2R
C;Superfamily: Saccharomyces cerevisiae hypothetical
                                                                                                                                                                   A;Reference number: Z25022
A;Accession: T49648
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-2298 <SCH>
A;Residues: 1-2298 <SCH>
A;Cross-references: UNIPROT:Q96U00; EMBL:AL355933; GS
A;Experimental source: BAC clone B8B20; strain OR74A
                                                                                                                                                                                                                                                                                                                                                            hypothetical protein B8B20.20 [imported] - Neurospora crassa C;Species: Neurospora crassa C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_cha C;Accession: T49648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: UNIPROT:P38338; EMBL:X70529; NID:g1907246; PIDN:CAA49923.1; R;Aigle, M.; Baclet, M.C.; Barthe, C.; Biteau, N.; Crouzet, M.; Doignon, F. submitted to the Protein Sequence Database, August 1994
A;Reference number: S45940
A;Accession: S46140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yeast 9, 189-199, 1993

A;Title: The complete sequence of a 19,482 bp segment located A;Reference number: S29348; MUID:93220397; PMID:8465606
A;Accession: S32961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Saccharomyces cerevisiae
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: S32961; S46140
R;Doignon, F: Biteau, N.; Crouzet, M.; Aigle, M.
Yeast 9, 189-199, 1993
                                                                                                                                                                                                                                                                                                                   R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; submitted to the Protein Sequence Database, May 2000
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C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-688 < AIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: translation not shown A;Molecule type: DNA A;Residues: 1-688 <DOI>
                                                                                                                                  ;Gene: NCSP:B8B20.20
          Matches
                            Query Match
Best Local :
                                                                                                                                                      Genetics
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                                                                                                            position:
                          Local Similarity
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les 67; Conserv
          114;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          126 ICKYGSIPPDVEEKLRLEWPYQEQLLLREHYQKKFKNSTYSRSS------VDVLYT 175
                                                                                         426/3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QDFAHIRSLKWDSNDKVESLIRALIFNDMFPYFNKEQVDTKADGIFFLRLLRKNFKEHIN 340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----NISWELGNEPNSFLKKA---DIF--INGSQLG--EDYIQLHKLLRK------
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        Conservative
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                       3.9%;
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79;
      Score 111; DB
Pred. No. 24;
79; Mismatches
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      190;
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                                           2; Length 2298;
                                                                                                                                                                                           GSPDB:GN00116; NCSP:B8B20.
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      Indels 208;
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FLTPSDSYSPPLQDPQLHTAGIMAYGVRLSEKDVPAASQLFWYLFNNFKVA 1957
                                                                     TLQLAMTNIKKDLFLLRSLALADPTASSTEEHRDYMAFTHGLIS-LIKSHGVGIVVVDSF
                                                                                                   RLPYPFSNKQVDKYLLRPLG-------PHGLLSKSVQLNGLTLKMVD--
                                                                                                                                            ATTPAPGVTSSASTAGSSSAQSIRRQREEFSH---
                                                                                                                                                                                                                IIKPMRFLGYETYLAEVLQQRGLPFLAEADVSAGMTPDYNIHLDLFSRAIHYMRKALRGG
                                                                                                                                                                                                                                                                                                                                                               PLKAITTFGKQTEQVACTEKTVTLAAKLAAR--
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                                                                                                                                                                                                                                                                                                                                                                                                                                    GWIETSSEEQYSSNESSADIDPRQLEDAILLLQEKLTKEFFWMA------RELLAL 1659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SW-ELGNEPNSFLKKADIFINGSOLGEDYIOLHKLLRKSTFKNAKLYGPDVGOPRRKTAK 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AS-LDVLKQAKTLEAAIYTLNVTQLQKMCTTLHFGSPGFDWGILNVAL-----DTHAHFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CSGLDLIFGLNAL-----LRTADLO------WNSSNAQLLLDYCSSKGYNI
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                                   -----DQTLPPLMEKPLRPG-----SSLGLPAFSYSF-FVIRNAKVA 540
                                                                                                                                                                                                                                                    LGLSAR-MGIEVVMRQVFFGAGNYHL--VDENFDPLPDYWLSL-LFKKLVG--TKVL---
                                                                                                                                                                                                                                                                                         KYGLFPDMPKNMSGPERRWL------PLFIATLVNKNVFDFKDIETNILSLWVQS 1755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QYMSAESDIEQQFRALSAENMRSIDAAWREELITKN------KATALDILHTSAR
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                                                                                                                                                                            ------MASVQGSK-----RRKLRVYLHCTNTDNPRYKEGDLTLYAINLHNVTKYL
                                                                                                                                                                                                                                                                                                                           K------KVWLGETSSAYGGGAPLLSDTFAAG-----FMWLDK 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---LEWPYQEQLLLREHYQKKFKNSTYSRSSVDVLYTFAN 178
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gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001

A,Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: E91031 Ş 밁 Ś A;Cross-references: UNIPROT:Q8XCP4; GB:BA000007; PIDN:BAB36644.1; PID:g13362691; GSPDB:GPA;Experimental source: strain O157:H7, substrain RIMD 0509952 probable outer membrane protein EC83221 [imported] - Escherichia coli (stra C;Species: Escherichia coli C;Species: Bull-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004 C;Accession: E91031 A; Residues: 1-879 < HAY> A; Molecule type: DNA E91031 A;Status: preliminary Query Match Best Local : Matches EC83221 112 FEERSYWQSQVNQDICKYGSIPPDVEEKL-----RLEWPYQEQLLLREHYQKKFKNS 163 130; 77 20 52 VSPSFLSVTIDANLATDPRFLILLGSPKLRTLARGLSPAYLRFGGTKTDFLIFDPKKEST 111 Similarity MSGSYVNAWAENEIQFDSRFLELKGDTKI-DLKRFSSQGYVEPG--KYNLQVQLNKQPLT EEYDIYWYASENDASKTYACLTPELVAQFGLKEDVAKNLQWIHDGKCLKPGQLE-----Conservative 3.9%; ; Score 109.5; ; Pred. No. 7.3; 68; Mismatches 208; DB 2; Escherichia coli (strain Indels 241; Length Gaps 130 76 33; 0157:H7, Han, and genon C.G.; 9

231 KKADIFINGSQLGEDYIQL	Qy 171 DVLYTFANCSGLDLIFGLNALLRTADLQWNSSNAQLLLDYCSSKGYNISWELGNEPNSFL 230	Qy 125 DICKYGSIPPDVEEKLRLEWPYQEQLLLREHYQKKFKNSTYSRSSV 170	Qy 90 AYLRFGGTKTDFLIFDPKKESTFEERSYWQSQVNQ 124	Qy 46 QEPLHLVSPSFLSVTIDANLATDPRFLILLGSPKLRTLARGLSP 89	Query Match 3.9%; Score 111.5; DB 2; Length 575; Best Local Similarity 21.4%; Pred. No. 2.7; Matches 72; Conservative 48; Mismatches 107; Indels 109; Gaps 19;	A;Gene: CWINV1 C;Superfamily: beta-fructofuranosidase C;Superfamily: beta-fructofuranosidase	A; MOLECULE CYPE: HIXMA A; Residues: 1-575 < WEBA A; Cross-references: UNIPROT: Q43855; EMBL: Z35162; NID: g861154; PIDN: CAA84526.1; PID: g8611 A; Experimental source: cv. Fribo, seed coat	Reference number: Z17416; MUID:96093423; PMID:8535137 Accession: T12094 Status: preliminary; translated from GB/EMBL/DDBJ	100000	ranosidase (EC 3.2.1.26) – fava bean Cia faba (fava bean) 1-1909 #semience revision 16-Tul-1009 #rext chan	Db 307 KIGKYLSTKQIKKGNIPEBILKIQKEDLNSSBIIKKMRLKF 347	247 IILAYKNPNFKPNRINEVDERVIALSVIALPYRDETLSLTKDKIIEDREERREKLKEKLI 30 430 KLRVYLHCTNTDNPRYKEGDLTLYAINLHNVTKYLRLPY 468	Db 203KEIYKRMEDNGVLISYSSAIPFRSALVDCGFVISEKESVGRKRG 246 OV 377 TEVVMROVEFGARNYHIVDENFDPIPDYWISILFKKINGTKVIMASVOGSKRR 429	259 KNAKLYGPDVGQPRRKTAKMLKSFLKAGGEVIDSVTWHHYYLNGRTATREDFLNPDVL 31	Qy 227 NSFL	Db 67 GALKEAIYKFAKPSKITDLSNPR-VLDLCSGMGYNAIAALHYNK 109	14 IRKYMKIYNGKNEKDIKERLIKELKEEHVLVETEDGTYTLKAEDEEEMMHSKV
SULT 7 2961 pothetical protein YBR; Alternate names: hypoth	Qy 524 LPAFSYSFEV 533 : : : Db 499 IPS-SYTSFI 507	Qy 469 PFSNKQVDKYLLRPLGPHGLLSKSVQLNGLTLKMVDDQTLPPLMEKPLRPGSSLG 523	Qy 421 -ASVQGSKRRKLRVYLHCTINTDNPRYKEGDLTLYAINLHNVTKYLRLPY 468 : : : : : : : : : : : : : : Db 407 RASLQAAEETDRKLKVYAVEKNPNAVVTLHNLVKMEGWEDVVTIISCDM 455	Qy 371 LSARMGIEVVMRQVFFGAGNYHLVDENFDDPWLSLLFKKLVGTKVLM 420	QY 311 LNPDVLDIFISSVQKVFQVVESTRPGKKVMLGETSSAYGGGAPLLSDTFAAGFMMLDKLG 370	Qy 254 RKSTFKNAKLYGPDVGQPRRKTAKMLKSFL-KAGGEVIDSVTWHHYYLNGRTATREDF 310	Qy 208 LDYCSSKGYNISWELGNEPNSFLKKA-DIFINGSQLGEDYIQLHKLL 253	Qy 162 NSTYSRSSVDVLYTFANCSGLDLIFGLNALLRTADLQWNSSNAQLL 207 :	Qy 108KESTFEERSYWOSQVNQDICKYGSIPPDVEEKLRLEWPYQEQLLLREHYQKKFK 161 : : : :	Qy 51 LVSPSFLSVTIDANLATDPRFLILLGSPKLTTLARGLSPAYLRFGGTKTDFLIFDPK- 107	Query Match 3.9%; Score 111; DB 2; Length 670; Best Local Similarity 22.4%; Pred. No. 3.7; Matches 123; Conservative 77; Mismatches 194; Indels 156; Gaps 33;	A;Gene: ATSP:F6E21.40 A;Map position: 4 A;Introns: 47/3; 87/1; 123/3; 203/3; 230/2; 255/3; 284/3; 305/1; 335/3; 347/3; 370/3; 39: C;Superfamily: Schizosaccharomyces pombe negative regulator of mitosis skbl	A; Molecule Cype: DAN A; Residues: 1-670 <bev> A; Cross-references: UNIPROT: Q9M090; EMBL: AL049914; GSPDB: GN00062; ATSP: F6E21.40 A; Experimental source: cultivar Columbia; BAC clone F6E21 C: Genetics:</bev>	or de t	hypothetical protein F6E21.40 - Arabidopsis thaliana C.Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004 C:Accession: T10666	RESULT 6	Db 506 GNNKKLSLIDHSVVESFGVGGKT 531

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hypothetical protein F13G24.30 - Arabidopsis thaliana (Species: Arabidopsis thaliana (Induse-ear cress) (C; Species: Arabidopsis thaliana (Induse-ear cress) (C; Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004 (C; Accession: T45608 R; Bevan, M.; Van Der Schueren, J.; Chuang, Y.J.; Voet, M.; Robben, J.; Volci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-521 <BEV>
A; Cross-references: UNIPROT: Q9SDA1; EMBL: AL133421
A; Experimental source: cultivar Columbia; BAC clo
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A; Introns: 53/3; 66/1; 127/2; 177/1; 256/1; 319/2; 361/2; 394/3
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A;Accession: T45608
A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δ
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Matches 154;
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                                                                        VSNGINVVLNAESRKKKSLLDTLKRPFSWIGSKASDGYLNREEYHLTPENGVLRSKTMVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LGSPKLRTLARGLSPAYLRFGGTKTDFLIFDPKKESTFEERSYWQSQVNQDICKYGSIPP 134
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                                   NGLTLKWVDDQTLPPLMEKPLRP-GSSLGLPAFSYSFFVIRNAKVAAC 542
                                                                                                                                             ALLWHRLMGKGVLAVQTDGPP--QLRVYAHCSK-----GRAGVTLLLINLSNQSDFTVS
                                                                                                                                                                             SLLFKKLVGTKVLMASVQGSKRRKLRVYLHCTNTDNPRYKEGDLTLYAINLHNVTKYL--
                                                                                                                                                                                                                 YNSGGRHVSDTFIDSFWYLDQLGMSARHNTKVYCRQTLVG-GFYGLLEKGTFVPNPDYYS
                                                                                                                                                                                                                                                                                      THHIYNLGSGNDPALVKKIMDPS----YLSQVSKTFKDVNQTIQEHGPWASPWVGESGGA
                                                                                                                                                                                                                                                                                                                         TWHHYYLNGRT--ATREDFLNPDVLDIFISSVQKVF----QVVESTRPGKKVWLGETSSA
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                                                                                                                                                                                                                                                                                                                                                                                                                                    GLNALRGRHKLRGKAWGGAWDHINTQDFLNYTVSKGYVIDSWEFGNELSG--SGVGASVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----PFQKM-----NSGLFGFSKGCLHMKRWDELNSFLTATGAVVTF
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     NGKSLKPTATGDIPSL-EPVLRSVNSPLNVLPLSMSFIVLPNFDASAC
                                                                                                                                                                                                                                                    YGGGAPLLSDTFAAGFMWLDKLGLSARMGIEVVMRQVFFGAGNYHLVDE-NFDPLPDYWL 406
                                                                                                        ---RLPYPFS---NKQVDKYLLRP---LGPHG--LLSKSVQL 495
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A; Note: T2L5.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Map position: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;Genetics:
                                                                      Query Match
Best Local (
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Matches 54;
                  126 ICKY---
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R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blak; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A. Science 273, 1058-1073, 1996

A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannasc A;Reference number: A64300; MUID:96337999; PMID:86880887

A;Accession: F64383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Accession: T01953
R;Geisel, C.; Smith, A.; Le, T.
submitted to the EMBL Data Library, October 1998
A;Description: The sequence of A. thaliana T2L5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein MJ0670 - Methanococcus jannaschii
C;Species: Methanococcus jannaschii
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: F64383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein T2L5.6 - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) (Space: 26-Feb-1999 #sequence_revision 26-Feb-1999)
                                                                                                                                                                                                     A; Map position: REV596956-595886
A; Start codon: GTG
                                                                                                                                                                                                                                                       A;Cross-references: UNIPROT:Q58084; GB:U67514; GB:L77117; C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Reference number: Z14470
A; Accession: T01953
                                                                                                                                                                                                                                                                                                               A;Residues: 1-356 <BUL>
                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                  A; Status: preliminary; nucleic acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Superfamily: Arabidopsis thaliana hypothetical protein T2L5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Experimental source:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: UNIPROT:O82604; EMBL:AF096371; NID:g3695386; PID:g3695392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Residues: 1-190 <GEI>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 6.0%;
Best Local Similarity 27.8%;
                                                                               / Match 4.0%; Score 112.5; DB 2;
Local Similarity 21.2%; Pred. No. 1.1;
nes 85; Conservative 48; Mismatches 143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            441 DNPRYKEGDLTLYAINLHNV------TKYLRLPYPFSNKQVDKYLLRPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YSFFVIRNAKVAAC 542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GPNGVIQREEYHLTAKDGNLHSQTMLLNGNALQVNSMGDLPPIBPIHINSTEPITIAPYS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RQSLIG-GNYGLLNTTNFTPNPDYYSALIWRQLMGRKALFTTFSGTK--KIRSYTHCA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ROVFFGAGNYHLVD-ENFDPLPDYWLSLLFKKLVGTKVLMASVQGSKRRKLRVYLHCTNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---ROSKG-ITVLLMNLDNTTTVVAKVELNNSFSLRHTKHMK----SYKRASSQLFG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6.0%; Score 169.5; DB 2; ilarity 27.8%; Pred. No. 2.5e-05; Conservative 34; Mismatches 57;
-GSIPPDVEEKLRLEWPYQEQLLLREHYQKKFKNSTYSRSSVD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cultivar Columbia
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                                                                                                                                                                                                                                                                                                                                                                     not shown; translation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels 49;
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                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       .; Woese, C.
jannaschii.
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Run on: OM protein - protein search, using sw model March 23, 2005, 11:19:33; Search time 27 Seconds (without alignments) 1935.026 Million cell updates/sec GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.

Title: Perfect score:

SEQ2A
2842
1 MLLRSKPALPPPLMLLLIGP.....LPAFSYSFFVIRNAKVAACI 543

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 283416 segs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seg length: 0
Maximum DB seg length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	897.5	31.6	480	2	JC7506	heparanase protein
N	4.	14.6	521	N	4560	ca
ω			190	N	T01953	ш
4	N		356	N	F64383	Р
v	•	3.9	575	N	T12094	fu
6	\vdash	ა •	670	N	T10666	hypothetical prote
7	111	3.9	688	N	S32961	•
89	111	3.9	2298	N	64	_
9	109.5	3.9	879	N	E91031	æ
10	108.5	ن. 8	411	N	S74760	ō
11	107.5		500	N	D87541	Ωı,
12	106	3.7	879	ν	F85875	probable fimbrial
13	105	3.7	670	N	T38446	microtubule-associ
14	104.5	3.7	788	μ	S00652	phosphoribosylamin
15	104	3.7	432	N	F70411	adenylosuccinate s
16	104	3.7	2013	N	AI1489	probable peptidogl
17	103.5	3.6	587	N	S36231	beta-fructofuranos
18	103.5	3.6	676	N	AF1153	transcription anti
19	103.5	3.6	687	N		retrotransposon li
20	103	3.6	796	2	D97065	
21	101	3.6	594	N	A82913	hypothetical prote
22	101	3.6	644	N	A97268	
23	100.5		805	N	H72098	•
24	•		805	N	C86525	
25	•		989	N	AE2140	toxin secretion AB
26			510	N	Н69893	conserved hypothet
27	99.5	5	837	ᆫ	A31842	,4-beta
28	99		897	N	G02529	dynein heavy chain
29	99	3.5	4644	ы	A38905	

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ALIGNMENTS

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Дb	Qy	Db	Qy	Ф	γQ	망	Qy	рb	Qγ	Дb	Qy	Query Ma Best Loo Matches	C; Comment: The therapies. C; Genetics: A; Gene: hpa2a A; Map positio C; Keywords: h	A; Refer A; Acces A; Molec A; Resid A; Cross	Biochem A;Title	C; Acces R; McKen	C;Species: C;Date: 17	RESULT JC7506	:
217 DAVTWQHCYIDGRVVKVMDFLKTRLLDTLSDQIRKIQKVVNTYTPGKKIWLEGVVTTSAG 276	291 DSVTWHHYYLNGRTATREDFLNPDVLDIFISSVQKVFQVVESTRPGKKVWLGETSSAYGG 350	157 MHGRAVNGSQLGKDYIQLKSLLQPIRIYSRASLYGPNIGRPRKNVIALLDGFMKVAGSTV 216	232 KADIFINGSQLGEDYIQLHKLLRK-STFKNAKLYGFDVGQPRRKTAKVLKSFLKAGGEVI 290	149DEPNNYRT 156	172 VLYTFANCSGLDLIFGLNALLRTADLQWNSSNAQLLLDYCSSKGYNISWELGNEPNSFLK 231	136 GGPGPD 148	112 FEERSYWQSQVNQDICKYGSIPPDVEEKLRLEWPYQEQLLLREHYQKKFKNSTYSRSSVD 171	78 FLSLQLDPSIIHD-GWLDFLSSKRLVTLARGLSPAFLRFGGKRTDFLQFQNLRNPAKSR- 135	56 FLSVTIDANLATDPRFLILLGSPKLRTLARGLSPAYLRFGGTKTDFLIFDPKKEST 111	18 PPACLAPGALYLALLHLSLSSQAGDRRPLPVDRAAGLKEKTLILLDVSTKNPVRTVNEN 77	20 PLGPLSPGALPRPAQAQDVVDLDFFTQEPLHLVSPS 55	<pre>Query Match 31.6%; Score 897.5; DB 2; Length 480; Best Local Similarity 36.0%; Pred. No. 9.2e-59; Matches 202; Conservative 74; Mismatches 146; Indels 139; Gaps 9;</pre>	C;Comment: This protein, a intracellular membrane-bound enzyme, has biological and therapies. C;Genetics: A;Gene: hpa2a A;Map position: 10q23-10q24 C;Keywords: heparin binding; membrane bound		Biochem. Biophys. Res. Commun. 276, 1170-1177, 2000 A;Title: Cloning and expression profiling of Hpa2, a novel mammalian heparanase family me	C;Accession: JC7506 R;McKenzie, E.; Tyson, K.; Stamps, A.; Smith, P.; Turner, P.; Barry, R.; Hircock, M.; Pat	iens #sec	1 ase protein 2a - human	

Matches	542; Conservative 1; Mismatches 0;	Indels 0; Gaps	0;
	1 MLLRSKPALPPPLMLLLLGPLGPLSPGALPRPAQAQDVVDLDFFTQEPLHLVSPSFLSVT	_	60
	1 MLLRSKFALPPPLMLLLLGPLGPLSPGALPRPAQAQDVVDLDFFTQEPLHLVSPSFLSVT	-	60
	61 IDANLATDPRFLILLGSPKLRTLARGLSPAYLRFGGTKTDFLIFDPKKESTFEERSYWQ		120
	61 IDANLATDPRFLILLGSPKLRTLARGLSPAYLRFGGTKTDFLIFDPKKESTFEERSYWQS		120
	121 QVNQDICKYGSIPPDVEEKLRLEWPYQEQLLLREHYQKKFKNSTYSRSSVDVLYTFANC	- to	180
	121 QVNQDICKYGSIPPDVEEKLRLEWPYQEQLLLREHYQKKFKNSTYSRSSVDVLYTFANCS		180
	181 GLDLIFGLNALLRTADLQWNSSNAQLLLLDYCSSKGYNISWELGNEPNSFLKKADIFINGS		240
	181 GLDLIFGLNALLRTADLQWNSSNAQLLLDYCSSKGYNISWELGNEPNSFLKKADIFING	ഗ —	240
	241 QLGEDYIQLHKLLRKSTFKNAKLYGPDVGQPRRKTAKMLKSFLKAGGEVIDSVTWHHYYL		300
	241 QLGEDFIQLHKLLRKSTFKNAKLYGPDVGQPRRKTAKMLKSFLKAGGEVIDSVTWHHYYL	-	300
	301 NGRTATREDFLNPDVLDIFISSVQKVFQVVESTRPGKKVWLGETSSAYGGGAPLLSDTFA		360
	301 NGRTATREDFLNPDVLDIFISSVQKVFQVVESTRPGKKVWLGETSSAYGGGAPLLSDTFA	-	360
	361 AGFMWLDKLGLSARMGIEVVMRQVFFGAGNYHLVDENFDPLFDYWLSLLFKKLVGTKVLM		420
	361 AGFMWLDKLGLSARMGIEVVMRQVFFGAGNYHLVDENFDPLPDYWLSLLFKKLVGTKVLM	_	420
	421 ASVQGSKRRKLRVYLHCTNTDNPRYKEGDLTLYAINLHNVTKYLRLPYPFSNKQVDKYLL	-	480
	421 ASVQGSKRRKLRVYLHCTNTDNPRYKEGDLTLYAINLHNVTF	YAINLHNVTKYLRLPYPFSNKQVDKYLL	480
	481 RPLGPHGLLSKSVQLNGLTLKMYDDQTLPPLMEKPLRPGSSLGLPAFSYSFFVIRNAKVA	-	540
	481 RPLGPHGLLSKSVQLNGLTLKNVDDQTLPPLMEKPLRPGSSLGLPAFSYSF	FVIRNAKVA	540
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Search completed: March 23, 2005, 11:25:48 Job time: 117.5 secs

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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                             heparanase, where the promoter and the region encoding human heparanase are operably linked in the exogenous polynucleotide such that human heparanase is expressed in at least a portion of the cells of the non-human animal. The methods and compositions of the present invention are useful for the production of transgenic animals expressing heparanase, to be used as models for human diseases such as cancers, viral infection, restenosis, neurodegenerative diseases, atherosclerosis and pulmonary consorters. The present sequence is human SK-hepl hpa protein used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New transgenic non-human animal expressing heparinase, useful as models for human disease, such as cancers, viral infection, neurodegenerative diseases, restenosis, atherosclerosis and pulmonary disorders.
                                                                                                                                                                                                                                                                                                                                                                                          Sequence 592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to a transgenic non-human animal whose genome comprises an exogenous polynucleotide sequence, including a promoter active in tissues of the non-human, a region encoding a human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zcharia E, 'Chajek-Shaul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ZCHA/)
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01-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                    exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (METZ/)
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)B; ADM48719, AD
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              301
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) CHAJEK-SHAUL T
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VLODAVSKY I.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     METZGER S.
                                                                                                                  GLDLIFGLNALLRTADLQWNSSNAQLLLDYCSSKGYNISWELGNEPNSFLKKADIFINGS
                                                                                                                                                                                                                                                                                         MILRSKPALPPPIMILLIGPLGPLSPGALPRPAQAQDVVDLDFFTQEPLHIVSPSFLSVT
NGRTATREDFLNPDVLDIFISSVQKVFQVVESTRPGKKVWLGETSSAYGGGAPLLSDTFA
                                                            QLGEDYIQLHKLLRKSTFKNAKLYGPDVGQPRRKTAKMLKSFLKAGGEVIDSVTWHHYYL
                                                                                                                                                          QVNQDICKYGSIPPDVEEKLRLEWPYQEQLLLREHYQKKFKNSTYSRSSVDVLYTFANCS
                                                                                                                                                                          QVNQDICKYGSIPPDVEEKLRLEWPYQEQLLLREHYQKKFKNSTYSRSSVDVLYTFANCS
                                                                                                                                                                                                                                  IDANLATDPRFLILLGSPKLRTLARGLSPAYLRFGGTKTDFLIFDPKKESTFEERSYWQS
                                                                                                                                                                                                                                                                            MILRSKPALPPPLMLLLLGPLGPLSPGALPRPAQAQDVVDLDFFTQEPLHLVSPSFLSVT
                                            QLGEDY1QLHKLLRKSTFKNAKLYGPDVGQPRRKTAKMLKSFLKAGGEVIDSVTWHHYYL
                                                                                                   GLDLIFGLNALLRTADLQWNSSNAQLLLDYCSSKGYNISWELGNEPNSFLKKADIFINGS
                                                                                                                                                                                                                    IDANLATDPRFLILLGSPKLRTLARGLSPAYLRFGGTKTDFLIFDPKKESTFEERSYWQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 14; 106pp; English.
                                                                                                                                                                                                                                                                                                                                 Conservative
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l T, Goldshmidt
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2001US-00776874.
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                                                   The invention relates to nucleic acid sequences that encode heparanase enzymes having endoglucuronidase activity. Recombinant heparanases are capable of removing the HS side chain from heparan sulfate proteoglycan (HSPG). Sulfated oligosaccharides, sulphonates or HSPG can be used to inhibit heparanase, this is useful for treatment of a physiological or medical condition associated with elevated heparanase activity, such as metastasis, angiogenesis, wound healing, angioplasty-induced restenosis, arteriosclerosis, atherosclerosis and inflammation. The human, murine and rat heparanases can be used to enhance wound healing, especially associated with tissue development and repair. The conditions mentioned above can be diagnosed using specific antibodies, and also using primers and probes specific for the heparanase polynucleotides. Other uses of the heparanases include sequencing sulfated molecules such as HSPG. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Heparanase; endoglucuronidase; heparan sulfate proteoglycan; enzyme; metastasis; angiogenesis; wound healing; angioplasty-induced resteno arteriosclerosis; atherosclerosis; inflammation; tissue development;
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                      The invention relates to an antisense oligonucleotide (ASO) comprising a CC polynucleotide or a polynucleotide analogue of at least 10 bases being CC hybridisable in vivo, under physiological conditions, with a portion of CC arealytic activity. Also included are method of in vivo downregulating CC heparanase activity (comprising administering the ASO in vivo), a method of treating a subject suffering from a pathological condition (c) characterised by heparanase activity, comprising administering the ASO in vivo), a method CC (characterised by heparanase activity, comprising administering ASO to the subject), a pharmaceutical composition comprising the ASO and a CC carrier, an antisense nucleic acid construct (comprising a promoter CC sequence and a polynucleotide sequence directing the synthesis of an CC carrier, and antisense conditions, with a polynucleotide strand encoding a CC contisense RNA sequence of at least 10 bases being hybridisable in vivo, compression to the conditions (comprising administering in vivo the compression the activity (comprising administering in vivo the antisense nucleic acid construct and a carrier, and an composition the antisense nucleic acid construct and a carrier, and an activity comprising the synthesis of an antisense nucleic acid construct and a carrier, and an activity comprising the antisense nucleic acid construct and a carrier, and an activity comprising the composition composition.
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                                                                     RPLGPHGLLSKSVQLNGLTLKMVDDQTLPPLMEKPLRPGSSLGLPAFSYSFFVIRNAKVA
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RESULT 14
ADM48720
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AC ADM48
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DT 03-JU
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DE Human
XX
reas
KW Trans
KW neurc
KW human
XX
Homo
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 Homo sapiens
                                            Transgenic animal; heparanase; cancer; viral infection; restenosis;
                                                                    Human SK-hep1
                                                                                                                  ADM48720
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                                  neurodegenerative disease;
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standard;

protein;

592 ₽

(first entry hpa protein

atherosclerosis;

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RESULT 12
ADG88804
ID ADG88
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AC ADG88
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DT 11-MA
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Matches 543; Conserv
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                 11-MAR-2004
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01-MAR-1999;
06-FEB-2001;
05-SEP-2001;
19-NOV-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human
                                                                                                                                                                                                                                                                                                                                    The present invention relates to methods and compositions for inducing and/or accelerating wound healing via the catalytic activity of heparanase. The invention is used to induce or accelerate a healing process, particularly of an ulcer, burn, laceration, surgical incision, necrosis, pressure wound, diabetic ulcer and to induce or accelerate angiogenesis. The present sequence is human SK-hepl protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Composition for treating a wound comprising recombinant useful to induce or accelerate wound healing and induce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB;
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            NGRTATREDFLNPDVLDIFISSVQKVFQVVESTRPGKKVWLGETSSAYGGGAPLLSDTFA
                                                         QIGEDYIQLHKLLRKSTFKNAKLYGPDVGQPRRKTAKMLKSFLKAGGEVIDSVTWHHYYL
                                                                                                   GLDL1FGLNALLRTADLQWNSSNAQLLLDYCSSKGYN1SWELGNEFNSFLKKAD1F1NGS
                                                                                                                                 QVNQDICKYGSIPPDVEEKLRLEWPYQEQLLLREHYQKKFKNSTYSRSSVDVLYTFANCS
                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 14; 143pp; English.
                                            QLGEDYIQLHKLLRKSTFKNAKLYGPDVGQPRRKTAKMLKSFLKAGGEVIDSVTWHHYYL
                                                                                      GLDLIFGLNALLRTADLQWNSSNAQLLLDYCSSKGYNISWELGNEPNSFLKKADIFINGS
NGRTATREDFLNPDVLDIFISSVQKVFQVVESTRPGKKVWLGETSSAYGGGAPLLSDTFA
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; 99US-00258892.
; 2001US-00776874.
; 2001WO-IL000830.
; 2001US-00988113.
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                                                                                                                                                                                                                                                                                Score 2842; DB 7;
Pred. No. 2.9e-273;
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or accelera
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                                                                                                        Best Local Similarity Matches 543; Conserv
                                                                                                                                      Query Match
                                                                                                                                                                                                           The specification describes a polypeptide having heparanase (hpa) activity. The recombinant protein is used as a modulator of heparin-binding growth factors, cellular responses to heparin-binding growth factors cellular responses to heparin-binding growth factors and cytokines, cell interaction with plasma lipoproteins, cellular susceptibility to viral, protozoal and bacterial infections or disintegration of neurodegenerative plaques. Heparanase may be useful for conditions such as wound healing, angiogenesis, restenosis, athersclerosis, inflammation, neurodegenerative diseases, and viral infections. Mammalian heparanase can be used to neutralize plasma heparin, and anti-heparanase antibodies may be applied for immunodetection and diagnosis of micrometastases, autoimune lesions, arrenal failure in biogsy specimens, plasma samples, and body fluids. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Heparanase; hpa; modulator; heparin-binding growth factor; cellular response; cytokine; cell interaction; plasma lipoprotein; cellular susceptibility; infection; disintegration; cellular susceptibility; infection; disintegration; neurodegenerative plaque; wound healing; angiogenesis; restenosis; athersclerosis; inflammation; neurodegenerative disease; neutralise;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A human heparanase
                                                                                                                                                                    Sequence 592 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAX35650.
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02-JUL-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             human polynucleotide useful for treating angiogenesis, restenosis,
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IDANLATDPRFLILLGSPKLRTLARGLSPAYLRFGGTKTDFLIFDPKKESTFEERSYWQS
                                                             MLLRSKPALPPPLMLLLLGPLGPLSPGALPRPAQAQDVVDLDFFTQEPLHLVSPSFLSVT
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                                            MLLRSKPALPPPLMLLLLGPLGPLSPGALPRPAQAQDVVDLDFFTQEPLHLVSPSFLSVT
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ilarity 100.0%;
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98US-00109386.
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                                                                                                        Score 2842; DB 2;
Pred. No. 2.9e-273;
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(HADA-)
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                                                                                                                                                                                                                                                                                                                           Human; heparanase; gene therapy; tumour; inflammation; autoimmunit heparin-binding growth factor; cytokine; neurodegenerative plaque; wound healing; infection; burn; angiogenesis; restenosis; atherosclerosis; inflammation; neurodegenerative disease;
                                                                                                                                                                                                                                                              WO200052178-A1
                                                                                                                                                                                                                                                                                                                 atherosclerosis; inflammation; neurodegenerative disease; Gerstmann-Straussler Syndrome; Creutzfeldt-Jakob disease.
                                                                                                                                                                                                                                                                                                                                                                                                Amino acid sequence of a human heparanase polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB08850;
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                                                                    WPI; 2000-579289/54
                                                                                             Pecker I,
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                                                                                                                       INSIGHT STRATEGY & MARKETING HADASIT MEDICAL RES SERVICES FRIEDMAN M M.
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New polynucleotides encoding a polypeptide having heparanase activity, useful in wound healing and in gene therapy, particularly in treating tumor, inflammation, autoimmunity, neurodegenerative diseases.

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                                                                                                                                                                                                                                                                                                                                                                                                     Transgenic animal; heparanase; cancer; viral infection; restenosis; neurodegenerative disease; atherosclerosis; pulmonary disorder; hpa
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    ZCHARIA E.
VLODAVSKY I.
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                                                                      ; 98WO-US017954.
; 99US-00258892.
; 2001US-00776874.
; 2001US-00988113.
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IDANLATOPRELILLGSPKLRTLARGLSPAYLRFGGTKTDFLIFDPKKESTFEERSYWQS

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GLDLIFGLNALLRTADI

241

NGRTATREDFLNPDVLDIFISSVQKVFQVVESTRPGKKVWLGETSSAYGGGAPLLSDTFA

360 360 300

AGFMMLDKLGLSARMGIEVVMRQVFFGAGNYHLVDENFDPLPDYWLSLLFKKLVGTKVLM

<u>AGFMWLDKLGLSARMGIEVVMRQVFFGAGNYHLVDENFDPLPDYWLSLLFKKLVGTKVLM</u>

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ASVQGSKRRKLRVYLHCTNTDNPRYKEGDLTLYAINLHNVTKYLRLPYPFSNKQVDKYLL

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Query Match
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Matches 543
                                                                                                                            The present invention relates to a transgenic non-human animal whose genome comprises an exogenous polynucleotide sequence, including a promoter active in tissues of the non-human, a region encoding a human heparanase, where the promoter and the region encoding human heparanase is expressed in at least a portion of the cells of the non-human animal. The methods and compositions of the present invention are useful for the production of transgenic animals expressing heparanase, the used as models for human diseases such as cancers, viral infection, restenosis, neurodegenerative diseases, atheroselerosis and pulmonary disorders. The present sequence is human hpa protein used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                             New transgenic non-human animal expressing heparinase, useful as models for human disease, such as cancers, viral infection, neurodegenerative diseases, restenosis, atherosclerosis and pulmonary disorders.
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Chajek-Shaul
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(PECK/)
(ILAN/)
(CHAJ/)
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B; ADM48715, AI
                                         al Similarity
543; Conserv
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ILAN N.
CHAJEK-SHAUL GOLDSHMIDT O.
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MLLRSKPALPPPLMLLLLGPLGPLSPGALPRPAQAQDVVDLDFFTQEPLHLVSPSFLSVT
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11 T, Goldshmidt
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Pred. No. 2.5e-273;
Pred. No. 0;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to methods and compositions for inducing and/or accelerating wound healing via the catalytic activity of heparanase. The invention is used to induce or accelerate a healing process, particularly of an ulcer, burn, laceration, surgical incision necrosis, pressure wound, diabetic ulcer and to induce or accelerate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Composition for treating a wound comprising recombinant useful to induce or accelerate wound healing and induce
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05-SEP-2001;
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DB; ADG88799, ADG88801,
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YACOBY-ZEEVI
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                                                     RPLGPHGLLSKSVQLNGLTLKMVDDQTLPPLMEKPLRPGSSLGLPAFSYSFFVIRNAKVA 540
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                                      RPLGPHGLLSKSVQLNGLTLKMVDDQTLPPLMEKPLRPGSSLGLPAFSYSFFVIRNAKVA
                                                                                          ASVQGSKRRKLRVYLHCTNTDNPRYKEGDLTLYAINLHNVTKYLRLPYPFSNKQVDKYLL
                                                                                                        ASVQGSKRRKLRVYLHCTNTDNPRYKEGDLTLYAINLHNVTKYLRLPYPFSNKQVDKYLL
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2001WO-IL000830.
2001US-00988113.
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Pred. No. 2.5e-273;
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                                                                                                                                                                  Catalytic activity. Also included are a method of in vivo downregulating conference activity. (comprising administering the ASO in vivo), a method conference and a subject suffering from a pathological condition conference activity. (comprising administering the ASO in vivo), a method conference activity a subject suffering from a pathological condition conference activity. Comprising administering ASO to contriber, an antisense nucleic acid construct (comprising a promoter conference and a polynuclectide sequence directing the synthesis of an antisense RNA sequence of at least 10 bases being hybridisable in vivo antisense RNA sequence of at least 10 bases being hybridisable in vivo conference and a polynucleotide sequence directing the synthesis of an accompany of an entod of in vivo conference and having heparanase catalytic activity), a method of in vivo conference antisense nucleic acid construct; a pharmaceutical composition comprising the antisense nucleic acid construct and a carrier, and an composition of at least 10 bases being hybridisable in vivo; under comprising the antisense nucleic acid construct and a carrier, and an composition of a polynucleotide strand being characterised by forming at least a portion of a polynucleotide strand being construct. The methods and compositions of the present invention are useful for the prevention and/or treatment of diseases or conditions associated with aberrant heparanase activity, such as per analysis activity.
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01-MAR-1999;
08-NOV-1999;
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                                                                         as heparanase-dependent cancer, cancer, autoimmune readinflammation. The gene for human heparanase is located The present sequence is a human heparanase protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hybridisable in vivo , under physiological conditions, with a portion a polynucleotide strand encoding a polypeptide having heparanase
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                     The invention relates to an isolated avian and reptile nucleic acid, encoding a polypeptide with heparanase catalytic activity. The signal peptide of the nucleic acid can be used to express membrane-associated secreted proteins in heterologous expression systems. The encoded polypeptides can be used to prevent tumour angiogenesis, metastasis and invasion, and to intervene with pathologies associated with impaired heparin-binding growth factors, cellular responses to heparin-binding
                                                                                                                                                                                                                                                                                                                 Nucleic acid encoding avian and reptile heparanase polypeptide is to treat various heparin-related disorders and the signal peptide useful in production of membrane-targeted or secreted recombinant
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                                                                                                                                                                                                                                    Disclosure; Fig 1a; 39pp; English
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                                                                                                                                                                                                                                                       Wound healing; heparanase; ulcer; burn; laceration; surgical incision; necrosis; pressure wound; diabetic ulcer; angiogenesis; human; therapy
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                                                    14-JAN-2003; 2003US-00341582.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence represents a heparanase of the invention. The heparanase DNA and protein sequences are useful in wound healing, angiogenesis, restenosis, atherosclerosis, inflammation, pulmonary diseases, and neurodegenerative diseases (such as Scrape, Alzheimer's disease, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence is particularly useful in gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           neurodegenerative diseases (such as Scrape, Alzl Creutzfeldt-Jakob disease) or viral infections.
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          The present sequence represents a human protein with heparanase cataly activity. The heparanase (hpa) polynucleotide is useful in gene therapy particularly in treating tumour, inflammation or autoimmunity. Particularly, the polynucleotide is useful in modulating the bioavailability of heparin-binding growth factors, cellular responses the partin-binding growth factors (e.g. bfGF) and cytckines (e.g. interleukin (IL)-8), cell interaction with plasma lipoproteins, cellular susceptibility to certain viral and some bacterial and protozoa infections, or disintegration of neurodegenerative plaques. The polynucleotide is also useful in wound healing (e.g. thermal, chemical radiation burns), and in the treatment of angiogenesis, restenosis, atherosclerosis, inflammation, neurodegenerative diseases (Gerstmann-Strausseler Syndrome or Creutzfeldt-Jakob disease), and some viral,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; heparanase; gene therapy; tumour; inflammation; autoimmunity; heparin-binding growth factor; cytokine; neurodegenerative plaque; wound healing; infection; burn; angiogenesis; restenosis; atherosclerosis; inflammation; neurodegenerative disease; Gerstmann-Straussler Syndrome; Creutzfeldt-Jakob disease.
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                          Human; heparanase; hpa; genetic modification; expression; anticancer; angiogenesis; anti-angiogenic; antiproliferative; antiviral; antitumou anti-atherosclerotic; anti-inflammatory; antineurodegeneration; heparan sulphate; heparin-binding growth factor; tumour angiogenesis; metastasis; wound healing; restenosis; atherosclerosis; inflammation; neurodegeneration; viral infection; cystic fibrosis; cancer; diagnosis micrometastasis; autoimmune lesion; kidney failure.
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CC The present invention describes genetically modified cells (A) containing CC a polynucleotide (I) that encodes a polypeptide with heparanase activity. CC and express recombinant heparanase (II). Heparanase cleaves heparan CC sulphate (HS) at specific intrachain sites, resulting in release of the parin-binding growth factors, enzymes and proteins that are sequestered by HS in basement membranes, extracellular matrix or cell surfaces. It CC may also be implicated in tumour angiogenesis and metastases. (II) is CC potentially useful in wound healing and for treating angiogenesis, createnosis, atherosclerosis, inflammation, neurodegeneration, viral CC infection and cystic fibrosis. It can also be used to neutralise heparin CC (an alternative to protamine) and to screen for specific inhibitors (potentially useful for treating cancer and metastases). Antibodies CC raised against (II) are used for immunodetection and diagnosis of CC micrometastases, autoimmune lesions and kidney failure. (A) provide (II) can large quantities, in a form that is homogeneously processed and CC activated/neutralised by a dedicated protease. The present sequence
                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                   Claim 3;
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Similarity

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OM protein - protein search, using sw model
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Run on: March 23, 2005, 11:09:57; Search time 113.5 Seconds (without alignments) 1850.316 Million cell updates/sec

Title: Perfect score: SEQ2A 2842

MLLRSKPALPPPLMLLLLGP...LPAFSYSFFVIRNAKVAACI 543

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters:

2105692 seqs, 386760381 residues

2105692

Minimum DB Maximum DB seq length: 0 seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:* geneseqp2002s:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. γď

SUMMARIES

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ALIGNMENTS

AAY02345 standard; protein; 543 A

AAY02345;

09-JUL-1999 (first entry)

A human heparanase protein.

Heparanase; hp; modulator; heparin-binding growth factor; cellular response; cytokine; cell interaction; plasma lipoprotein; cellular susceptibility; infection; disintegration; neurodegenerative plaque; wound healing; angiogenesis; restenosis; athersclerosis; inflammation; neurodegenerative disease; neutralise plasma heparin; micrometastasis; autoimmune lesion; renal failure. neutralise;

Homo sapiens.

WO9911798-A1

11-MAR-1999.

31-AUG-1998; 98WO-US017954.

02-SEP-1997; 02-JUL-1998; 97US-00922170. 98US-00109386.

(INSI-) INSIGHT STRATEGY & MARKETING (HADA-) HADASIT MEDICAL RES SERVICES (FRIE/) FRIEDMAN M M. & DEV.

Pecker I, Vlodavsky I, Feinstein

N-PSDB; AAX35648 WPI; 1999-302255/25.

New human polynucleotide and inflammation. useful for treating angiogenesis, restenosis

Claim 6; Fig 1; 63pp; English.

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CC Cellic The specification describes a polypeptide having heparanase (hp) activity. The recombinant protein is used as a modulator of heparin-binding growth factors, cellular responses to heparin-binding growth factors and cytokines, cell interaction with plasma lipoproteins, cellular susceptibility to viral, protozoal and bacterial infections or disintegration of neurodegenerative plaques. Heparanase may be useful for

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01-MAy-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein F13G24.30.
Name=F13G24.30.
                                                                                                                                                                                                                       EU Arabidopsis sequencing project;

Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AL133421; CAB62595.1; -.

PIR; T45608; T45608.

InterPro; IPR001199; Glyco_hydro_79N.

InterPro; IPR001254; Peptidase_SI.

Pfam; PF03662; Glyco_hydro_79n; 1.

PROSITS; PS00135; TRYPSIN_SER; UNKNOWN_1.

Hypothetical protein.

SEQUENCE 521 AA; 57831 MW; 07D8664A4B305CC2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

Bevan M., Van Der Schueren J., Chuang Y.J., Voet M., Robben J., Volckaert G., Bancroft I., Mewes H.W., Lemcke K., Mayer K.F.X.; Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosid
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                             Local Similarity
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                                                        LGSPKLRTLARGLSPAYLRFGGTKTDFLIFDPKKESTFEERSYWQSQVNQDICKYGSIPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YY--ESNLHNLRPNIHRYGRYVSLPPYSIGFWVIKKTSITVC 514
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LGETSSAYGGGAPLLSDTFAAGFMWLDKLGLSARMGIEVVMRQVFFGAGNYHLVDENFDP
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LTRPLLTKAIKAFKPLRIRIGGSLQDQVIYDVGNLKT---
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                                                                                                                Conservative
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                                                                                                                68;
                                                                                                                                          Score 416; DB 2;
Pred. No. 1.6e-22;
                                                                                                                Mismatches 184;
                                                                                                                                                                     Length 521;
                                                                                                                Indels 122;
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                                                                                                                                                                                                                                                                                                                                 GSQLGEDYIQLHKLLRKSTFKNAKLYGPDVGQP-----RKKTAKMLKSFLKAGGEVIDSV
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NGKSLKPTATGDIPSL-EPVLRSVNSPLNVLPLSMSFIVLPNFDASAC 520
                                                           VSNGINVVLNAESRKKKSLLDTLKRPFSWIGSKASDGYLNREEYHLTPENGVLRSKTMVL
                                                                                                                                                       SLLFKKLVGTKVLMASVQGSKRRKLRVYLHCTNTDNPRYKEGDLTLYAINLHNVTKYL--
                                                                                                                                                                                                                                                  THHIYNLGSGNDPALVKKIMDPS----YLSQVSKTFKDVNQTIQEHGPWASPWVGESGGA
                                                                                                                                                                                                                                                                                                                                                                            GLNALRGRHKLRGKAWGGAWDHINTODFLNYTVSKGYVIDSWEFGNELSG--SGVGASVS
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                          NGLTLKMVDDQTLPPLMEKPLRP-GSSLGLPAFSYSFFVIRNAKVAAC
                                                                                                                       ALLWHRLMGKGVLAVQTDGPP--QLRVYAHCSK-----GRAGVTLLLINLSNQSDFTVS
                                                                                                                                                                                                                  YGGGAPLLSDTFAAGFMWLDKLGLSARMGIEVVMRQVFFGAGNYHLVDB-NFDPLPDYWL
                                                                                                                                                                                                                                                                                  TWHHYYLNGRT--ATREDFLNPDVLDIFISSVQKVF----QVVESTRPGKKVWLGETSSA
                                                                                                                                                                                      YNSGGRHVSDTFIDSFWYLDQLGMSARHNTKVYCRQTLVG-GFYGLLEKGTFVPNPDYYS
                                                                                                                                                                                                                                                                                                                                                                                                -WNSSNAQLLLDYCSSKGYNI-SWELGNEPNSFLKKADIFIN 238
                                                                                          RLPYPFS---NKQVDKYLLRP---LGPHG--LLSKSVQL
                                                                                                                                                                                                                                                                                                                                                                                                                                            ----NSGLFGFSKGCLHMKRWDELNSFLTATGAVVTF 132
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                                                                                                                                                                                                     McKenzie E.A., Tyson K., Stamps A.; Submitted (JUN-2000) to the EMBL/GenBank/DDbJ EMBL; AF282885; AAG23421.1; -
PIR; JC7506; JC7506.
InterPro; IDR005199; Glyco_hydro_79N.
Pfam; PF03662; Glyco_hydro_79n; 1.
SEQUENCE 480 AA; 53900 MW; F75F89F67AC1FF8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

MEDLINE=20483645; PubMed=11027606; DOI=10.1006/bbrc.2000.3586;

MCKenzie E., Tyson K., Stamps A., Smith P., Turner P., Barry R.

Hircock M., Patel S., Barry E., Stubberfield C., Terrett J., Pa

"Cloning and expression profiling of Hpa2, a novel mammalian
heparanase family member.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation updat
Heparanase-like protein HPA2a.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biochem. Biophys.
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PPACLAPGALYLALLHLSISSQAGDRRPLPVDRAAGLKEKTLILLDVSTKNPVRTVNEN
                                              PLGPLSPGAL------PRPA-----QAQDVVDLDFFTQEPLHLVSPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Res. Commun.
                                                                                                                                 31.6%; Score 897.5; 36.0%; Pred. No. 9.4
                                                                                                     74;
                                                                                                                                                                                                           F75F89F67AC1FF83 CRC64;
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                                                                                                        Mismatches 146;
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                                                                                                                                      Query Match
Best Local S
Matches 183
                                                                                                                                                                                                                                                                         STRAIN=p50; TISSUE=Posterior silkgland;
Kolke Y., Mita K., Suzuki M.G., Maeda S., Abe H., Osoegaw
A deJong P.J., Shimada T.;
Genomic sequence of a 320-kb segment of the Z chromosome
mori containing a kettin ortholog.";
Mol. Genet. Genomics 269:137-149(2003).
EMBL; AB079860; BAB85191.1;
EMBL; AB079860; BAB85191.1;
EMBL; AB090307; BAC10612.1;
EMBL; AB090307; BAC1061
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Bombyx mori (Silk moth).

Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bom

Bombycidae; Bombyx.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2002 (TrEMBLrel. 21, 01-JUN-2002 (TrEMBLrel. 21, 05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=Bmhepa;
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                                                                                                                                          Conservative
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                                                                                                                                                                        24.5%;
                                                                                                                                      83;
                                                                                                                                  Score 696; DB 2; L
Pred. No. 1.4e-43;
33; Mismatches 182;
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Q8WWQ1;
01-MAR-2002
01-MAR-2002
01-JUN-2003
                                                                                                                                           TISSUE-Prostate;
Pesseque Safontas B.J.O.P.S.;
Pesseque Safontas B.J.O.P.S.;
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ
EMBL; AJ299720; CAC82492.1; -.
Pfam; PF03662; Glyco_hydro_79n; 1.
SEQUENCE 548 AA; 61771 MW; B8986303FC73A6(
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
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Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                               Legoux P., Legoux R.,
Submitted (JAN-2002)
                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chordata;
                                                               35.7%; Score 1015.5; DB 2;
41.8%; Pred. No. 1.6e-67;
tive 79; Mismatches 180;
                                                                                                                                                                                                                                                                                                                               , O'Brien D., Salome M.;
to the EMBL/GenBank/DDBJ databases
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                      B8986303FC73A60A CRC64;
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Q9HB38;
Q1-MAR-2001
                                                                                                                                                                          SEQUENCE FROM N.A.

MCKENTAIE E.A., TYSON K., Stamps A.;

Submitted (JUN-2000) to the EMBL/GenBank/DDBJ database;

EMBL; AF282886; AAG23422.1; -...

InterPro; IPR005199; Glyco_hydro_79n; 1.

Pfam; PF03662; Glyco_hydro_79n; 1.

SEQUENCE 534 AA; 60063 MW; C3DE5E900CB338C4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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01-MAR-2001 (TYEMBLYE1. 16, La
01-MAR-2004 (TYEMBLYE1. 26, La
Heparanase-like protein HPA2b.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIINE=20483645; PubMed=11027606; DOI=10.1006/bbrc.2000.3586; MCKENZIE E., Tyson K., Stamps A., Smith P., Turner P., Barry R. Hircock M., Patel S., Barry B., Stubberfield C., Terrett J., P. "Cloning and expression profiling of Hpa2, a novel mammalian
                                                                                                                                                                                                                                                                                                                                                                                               Biochem. Biophys.
                                                                                                                                                                                                                                                                                                                                                                                                                            "Cloning and expression profiling of Hpa2, heparanase family member.";
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                                                                                            Local Similarity
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                                                               33.0%; Score 936.5; DB 2; 37.8%; Pred. No. 1.3e-61; tive 78; Mismatches 168;
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16, Last sequence update)
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                                                                                McKenzie E.A., Tyson K., Stamps A.;
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ
EMBL; AF282887; AAG23423.1;
GO; GO:0005622; C:intracellular; TAS.
GO; GO:0030305; F:heparanase activity; TAS.
InterPro; IPR005199; G1yco_hydro_79N.
Pfam; PF03662; G1yco_hydro_79n; 1.
SEQUENCE 592 AA; 66580 MW; 95C384AD9A74258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Heparanase-like protein HPA2c.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9НВ37
Q9НВ37;
                                                                                                                                                                                                                                                                                                                                 MEDLINE=20483645; PubMed=11027606; DOI=10.1006/bbrc.2000.3586; MCKenzie E., Tyson K., Stamps A., Smith P., Turner P., Barry R. Hircock M., Patel S., Barry E., Stubberfield C., Terrett J., P. "Cloning and expression profiling of Hpa2, a novel mammalian heparanase family member.";
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                                                                                                                                                                                                                                                                                                              Biochem.
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      Conservative
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                      Score 1154.5;
Pred. No. 6.3e
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                                                                                    95C384AD9A74258E CRC64;
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                         6.3e-78;
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                                           DB 2;
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AC QBWWQ
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OS Homo
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Query Match
Best Local S
Matches 249
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Q8WWQ2;
Q1-MAR-2002 (TrEMBLrel. 20,
Q1-MAR-2002 (TrEMBLrel. 20,
Q1-MAR-2003 (TrEMBLrel. 23,
                                                                                                           Pessegue Safontas B.J.O.P.S.;
Submitted (SEP-2000) to the EM
EMBL; AJ299719; CAC62491.1; -.
Genew; HGNC:18374; HPSE2.
Pfam; PF03662; Glyco_hydro_79n
                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
TISSUE=Prostate;
Legoux P., Legoux R.,
Submitted (JAN-2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                 Heparanase 2.
Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, E
Mammalia, Eutheria, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                             TISSUE=Prostate;
                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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    Conservative
                                                                                          Glyco_hydro_79n;
AA; 66520 MW;
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40.3%; Score 1146.5; DB 2; 43.4%; Pred. No. 2.5e-77; tive 82; Mismatches 190;
                                                                                                                                                                                                                                                                                              'Brien D., Salome M.; the EMBL/GenBank/DDBJ
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                                                                                                                                                                                     EMBL/GenBank/DDBJ
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9478841FEACD558B
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                                                                                          CRC64;
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Gaps
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                                                                                                                                                                                                                                                                                                                    Q9QZF8
Q9QZF8;
01-MAY-2000
01-MAY-2000
01-JUN-2002
SEQUENCE FROM PODYMA K.A., Submitted (SI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
Hulett M.D., Wang J.,
Parish C.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (MAR-2001) to the EMBL/GenBank/DDBJ
                                                                            SEQUENCE FROM N.A.

MEDLINE=22194309; PubMed=12077130; DOI=10.1074/jbc.M203282200;

MEDLINE=27194309; PubMed=12077130; DOI=10.1074/jbc.M203282200;

Podyma-Inoue K.A., Yokote H., Sakaguchi K., Ikuta M., Yanagishita M

Podyma-Inoue K.A., Yokote H., Sakaguchi K., Ikuta M., Yanagishita M

"Characterization of heparanase from a rat parathyroid cell line.";

J. Biol. Chem. 277:32459-32465(2002).
                                                                                                                                                                                                                     Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                             Heparanase.
Name=Hep;
                                                                                                                                                                                                NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             302
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Pred. No. 1
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Interpro; IPR005199; Glyco hydro
Pfam; PF03662; Glyco hydro 79n; I
SEQUENCE 536 AA; 60568 NW; 63
                                                                                                                      SEQUENCE FROM N.A.

MEDLINE=21369959; PubMed=11387326; DOI=10.1074/jbc.M102462200;

Goldshmidt O., Zcharia E., Aingorn H., Guatta-Rangini Z., Atzm

Goldshmidt O., Pecker I., Mitrani E., Vlodavsky I.;

Michal I., Pecker I., Mitrani E., Vlodavsky I.;

"Expression pattern and secretion of human and chicken heparan

determined by their signal peptide sequence.";

J. Biol. Chem. 276:29178-29187(2001).
                                                                                  EMBL;
Pfam;
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Gallus gal
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Archosauria; Aves;
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                                                              AY037007; AAK82648.1; -.
PF03662; Glyco_hydro_79n;
NCE 523 AA; 58386 MW; 8
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RESULT Q6YGZ1
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EMBL; AX040471; BAC30600.1; -.
EMBL; AR359507; AAQ15188.1; -.
MGD; MGI:1343124; Hpse.
GO: GO:0005578; C:extracellular matrix (sensu Me InterPro; IPR005199; G1yco_hydro_79N.
9fam; PF03662; G1yco_hydro_79n; 1.
SEQUENCE 535 AA; 60065 MW; 6E73A8302FB8A0DF
                                                         Q6YGZ1;
Q6YGZ1;
05-JUL-2004
05-JUL-2004
05-JUL-2004
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Hulett M.D., Wang J.,
Parish C.R.;
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                           Mus musculus (Mouse)
Eukaryota; Metazoa;
                                       Heparanase.
Mus musculu
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TISSUE=Spleen;
J., Hornby J.R.,
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                 Eutheria;
                                                         (TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
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                                                                                                    PRELIMINARY;
                 Chordata;
Rodentia;
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76.6%;
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Pred. No. 8.9e
51; Mismatches
                                                         Created)
Last sequence update)
Last annotation update)
                Craniata; Vert
Sciurognathi;
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No. 8.9e-153;
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                            Vertebrata; Euteleostomi;
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                 Muridae;
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RESULT Q71RP1 ID Q71RP1 AC Q71 AC Q7 DT Q5                                                                                                                                                                                                                                                                                                                                                                                           유상유
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Best Local S
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Q71RP1;
Q5-JUL-2004
05-JUL-2004
05-JUL-2004
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10116;
                                                                               Heparanase.
Name=Hspe;
Rattus norvegicus
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Submitted (SEP-2002) to the EMBL/GenBan

EMBL; AY151051; AAN41636.1; -.

GO; GO:0005578; C:extracellular matrix

InterPro; IPR005199; Glyco hydro 79N.

Pfam; PF03662; Glyco hydro 79n; I.

SEQUENCE 535 AA; 59992 MW; 3748AEB3
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SEQUENCE FROM N.A.
MEDLINE=22841152; PubMed=12837765; DOI=10.1074/jbc.M300925200;
Gong F., Jemth P., Galvis M.L.E., Vlodavsky I., Horner A., Lin
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76.6%; Pred. No. 5e-15:
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                                          Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
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01-JUN-2001 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
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"Expression of heparanase mRNA in
Reproduction 121:573-580(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bos taurus (Bovine).
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InterPro; IPR005199; Glycc_hydro_79N; 1.
Pfam; PF03662; Glyco_hydro_79n; 1.
SEQUENCE 545 AA; 61076 MW; FAC4BE
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Last annotation updat
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Pred. No. 1.1e-162;
5; Mismatches 73;
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n bovine placenta during
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PRESENTATION OF THE PROPERTY O
SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SETRAIN=C57BL/6J; TISSUE=Thymus;

STRAIN=C57BL/6J; TISSUE=Thymus;

STRAIN=C57BL/6J; TISSUE=Thymus;

STRAIN=C57BL/6J; TISSUE=Thymus;

Haza A., Hashizume W.,

Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,

Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,

Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Kasukawa T.,

Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,

Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Kol

Katoh H., Kawai J., Kojima Y., Miyazaki A., Murata M., Nakamura M.,
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STRAIN=FVB;
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STRAIN-C57BL/6J; TISSUE=Thymus;

MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;

Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;

"Normalization and subtraction of cap-trapper-selected cDI prepare full-length cDNA libraries for rapid discovery of Genome Res. 10:1617-1630(2000).
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01-CCT-2002 (TrEMBLrel. 22, Created)
01-CCT-2002 (TrEMBLrel. 22, Last sequence update)
25-CCT-2004 (TrEMBLrel. 28, Last annotation update)
Heparanase (Mus musculus 0 day neonate thymus cDNA,
enriched library, clone:A430101M04 product:heparanase
                                                                                                                                                                                                                                                                                                                                                                                      sequencing progressing sequencing for the sequencing sequences for the sequences for the sequences for the sequences for the sequencing progression for the
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MEDLINE=20530913; PubMed=11076881; DOI=10.1101/gr.152600;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
MIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer.";
Genome Res. 10:1757-1771(2000).
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STRAIN=C57BL/6J; TISSUE=Thymus;
MEDLINE=21085660; PubMed=11217851;
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STRAIN=C57BL/6J; TISSUE=Thymus;
MEDLINE=99279253; PubMed=10349636;
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SEQUENCE FROM
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STRAIN=C57BL/6J; TISSUE=Thymus;
The FANTOM Consortium,
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"High-efficiency full-length cDNA cloning.";
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 420:563-573 (2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Enzymol.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chordata;
Rodentia;
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se, full insert
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A Spector L., Pecker I.;

A Spector L., Pecker I.;

Submitted (ApR-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AF165154; AAD45669.1; -.

R EMBL; AF155376; AAD45669.1; -.

R EMBL; AF155310; AAD54941.1; -.

R EMBL; BC051321; AAD54941.1; -.

R EMBL; BC051321; AAD41342.1; -.

R EMBL; BC051321; AAD41342.1; -.

R EMBL; BF144325; AAD41342.1; -.

R EMBL; BF1065199; Proteoglycan metabolism; TAS.

R GO; GO:0004566; F:beta-glucuronidase activity; TAS.

R GO; GO:0006029; P:proteoglycan metabolism; TAS.

R InterPro; IPR005199; Glyco_hydro_79N.

R Ffam; PF03662; Glyco_hydro_79n; T

CHAIN

SEQUENCE 543 AA; 61176 MW; AD262EC267334AB2 CRC64;
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Best Local Similarity
Matches 542; Conserv
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Ishai-Michaeli R., Bita
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., Pappo O., Peretz
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EMBL; AF084467; AAD54516.1; -.

Genew; HGNC:5164; HPSE.

InterPro; ITR005199; Glyco_hydro_79N.

Pfam; PF03662; Glyco_hydro_79n; 1.

SEQUENCE 545 AA; 61417 MW; 67B80ACD73C5A9A1
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TISSUE-Placenta;
MEDLINE=20229546; PubMed=10764835; DOI=10.1093/glycob/10.5.467;
Dempsey L.A., Plummer T.B., Coombes S.L., Platt J.L.;
"Heparanase expression in invasive trophoblasts and acute vascu
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Mammalia; F
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Eutheria; Primates;
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   1645.5
1154.5
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seq length: 2000000000
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   GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
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              08K3K3
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071RP1
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09QZF8
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                                                                                                                                                                                                                                                                                                                                     Q9Y251
Q9UL39
                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1612378
Ogmyyo bos taurus
Ogkaka mus musculu
Ogygzi mus musculu
Ofygzi mus musculu
Oflrp1 rattus norv
Ogogzi rattus norv
Ogogzi rattus spien
Ogwaqa homo sapien
Ogwaqa homo sapien
Oghbay homo sapien
Oghida arabidopsis
Oglica arabidopsis
Oglica arabidopsis
Oglica arabidopsis
Oglica arabidopsis
Oglica arabidopsis
Oglica arabidopsis
Ogvero drosophila
Orstbo neurospora
Ofster burkholderi
Oghkol thermoplasm
Oghezl phanerochae
                                                                                                                                                                                                                                                                                                                                    Q9y251 homo sapien
Q9ul39 homo sapien
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Result No.

ALIGNMENTS

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Whiting M., Madan A., Young A.C., Shevchenko Y., Bourtard G.G.,	hey J., Helton E., Ketteman M., Madan A., Rodrigues S.,	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,	McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.	.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy	J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,	Casavant T.L., So	f. Marisina K. Farmer A.A. Rubin G.M. Hong L.	B F .Tordan H Moore T Max S I . Wang J . Haigh F.	B Bustow K H Schaefer C F Bhat N K	B D Colling F & Wagner I. Shenmen C M. Schiller G D	Feincold E A Grouse I H Derge I G	MEDITATE=2032880577: D::Med-12477932: DOT-10 1073/pnag 242603899:	SECUENCE FROM N.A.	E NOR	J. Biol. Chem. 274:24153-24160(1999).		nase. Purifi	alima M.:	MEDLINE=99377052: PubMed=10446189: DOI=10.1074/ibc.274.34.24153;		chem. Biophys. Res. Commun. 261:183-187(19)	and functional expression of a human	.P., Giorgio N.A., Bohlen P.;	es J.D., Ludwig D.L., Patel S., Navarro E.C.	; PubMed=10405343; DOI=10.1006/bbrc.1999.	lacenta;	SECTION OF A SECTI	. Med. Dio	E HOLES	of mammalian hep	.R.;	3	; PubMed=10395326	lacenta:	CEOTIFICE FROM N A	D=9606;	Eutheria; Primates; Catarrhini; Hominidae;	a; Craniata; V	syn	e.	(TrEMBLrel.	ted)		2 H	ն 1

Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension .rup) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

http://www.pir.uniprot.org/database/archive.shtml

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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